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Minimum DB seq length: 0
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-031-555-10
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US-08-928-3618-6
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                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,221
FILING DATE: 20-FEB-1991
APPLICATION NUMBER: 73440/1990
FILING DATE: 26-MAR-1990
FEATURE:
                  MOLECULE TYPE: protein
                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                      FILING DATE: 26-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compa
OPERATING SYSTEM: MS DI
SOFTWARE: ASCII FORM
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 0.72 mb
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APPLICANT: Kawamura, Yoshiya
TITLE OF INVENTION: Structural Gene of Membrane-Bound
TITLE OF INVENTION: Alcohol Dehydrogenase Complex, Plasmid
TITLE OF INVENTION: Containing The Same And Transformed Acetic Acid
TITLE OF INVENTION: Bacteria
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ADDRESSEE: Frishauf, Holtz, Goodman & Woodward, P.C
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APPLICANT:
                                                                                                                     TELLEFAX: \_
TELEFAX: \_
Tex: 236268
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                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 Third Avenue
                                                                                                                                                       (212)370-1622
                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukaya, Masahiro;
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AUTHORS: Tamaki, Toshimi;
AUTHORS: Fukaya, Masahiro
                                        497
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                                                                                                                                                                 411
                                                                                                                                                                                                   389 DAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQEFT-SMDVY 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGES: 292-300
DATE: 1991
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LFQGLANGEFHAYDATNGSDLFHFAADSGIIAPPVTYLANGKQYVAVEVG
                                    LFNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAIAGG 546
                                                                               NLGLDMNKVGTPDSPEAKQAFVKDLKGWTVAWDPQKQAEAWRVDHKGPWNGGTLATGGDL
                                                                                                                                                            DALYTLTGKEWYGIPGDLGGHNFAAMAFSPKTGLVYIPAQQVPFLYTNQVGGFTPHPDSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGTICAALISGYATMASADDGQGATGEAIIHADDHPGNWMTYGRTYSDQRYSPLDQINR 76
                                                                                                                    NTS---NVTKLPPG-----KDMIGRIDAIDISTGRTLWSVERAAANYSPVLSTGGGV 496
                                                                                                                                                                                                                                              -----NGETRHVIVHARKNGFFYIIDAKTGEFISGKNYVYVNWASGLDPKTGRPIYNP 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIADKGCCDTVNRGAAYWNGKVYFGTFDGRLIALDAKTGKLVWSVNTIPPEAELGKQRSY 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SSGPIVANGVIVAGSTCQYSPFGC--FVSGHDSATGEELWRNYFIPRAGEEGD-----
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Cloning and Sequencing of the Gene Cluster
Encoding Two Subunits of Membrane-Bound
Alcohol Dehydrogenase from Acetobacter
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Tayama, Kenji;
Okumura, Hajime;
Kawamura, Yoshiya;
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Horinouchi, Sueharu and
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36 to 738
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APPLICANT: HOSHINO, Tatsuo APPLICANT: MIYAZAKI, Taro

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; ORGANISM: Gluconobacter suboxydans
US-09-296-284-25
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; Sequence 2, Application US/09136251A
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CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
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APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of Use Thereof
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                                                                                                                                                                                         521 RLATVASGQAISYEVDGMQYVAI----AG-----GGVSYGSG 553
                                                                                                                                                                                                                                          462 LKGWIVAWDPQKQQAAFTVDHKGPWNGGLLATAGGVLFQGLANGEFHAYDATTGKDLFTF 521
                                                                                                                                                                                                                                                                                                                                          402
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                                                                                                                                                                                                                                                                                       MIGRIDAIDISTGRTLWSVERAAANYSPVLSTGGGVLFNGGTDRYFRALSQETGETLWQT 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETGEFLWARDTNYQNMIESIDE-NGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALN 417
                                                                                                                                              PAQSAIIAPPVTYTANGKQYVAVEVGWGGIYPFFLGGVARTSG
                                                                                                                                                                                                                                                                                                                                        PQTKLVYIPAQQVPFVYDPQKGGFKAHHDSWNLGLDMNKIGLLDDNDPQHKADKAQFLKD 461
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GENERAL INFORMATION:

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; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
US-09-136-251-2
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NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
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Best Local Similarity
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APPLICANT: SHINJOH, Masako
APPLICANT: TOMIYAMA, No. 6127156ibumi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 VDVQPSTEMEGLQSINPNAATGERRVLTGVPCKTGTMWQFDAETGEFLWARDTNYQNMIE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 -----AWDVNNSGR------SQPAY-RVTVITAVERRIPGLPDRRQRG------GSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 ESVPGFVSMTAPPPVINGVVVVNHEVLDGQRRWAPSG-VIRGYDAESGKFVW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 EDM---VSNSSGPIVANGVIVAGSTC-----QYSPFGCFVSGHDSATGEELWRNYFIPRA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 TYFTSSVVPEGQPCHNRLIEGT-----LDMRLIAVDAETGDFCPNFGHGGQVNLMQGLG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 ------GEPTRGMALYGTNVYFVSWDNHLVALDTATGQV-----TFDVDRGQG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 QVNKWAAETTPIKVGDGLYTCSAMNDIIK-LDPATGKQIWRRNVDVKYHSIPYTAACKGV 204
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                       505 YFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAIAGGGVSYGSGLNSALAGERVD 564
                                                                     615 TAIDMKHGQKVLWQHPLGTARANGPWGLPTGLPWEIGTPNNGGSVVTGGGLIFIGAATDN 674
                                                                                                                    466 DAIDISTG-RTLWS------VERAAANYSPVLSTGGGVLFNG-GTDR 504
                                                                                                                                                                        560 DSLGLMPIDDPNFKPGGGGAEGNGAMDGTPYGIVVTPFWDQY-TGMMCNRPP----YGMI
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                                                                                                                                                                                                                                                                                                              -----VEYDVCPTFLGGRDWPSAALNPDSGTYFIPLN-NVCYDMMAVDQEF 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91; Mismatches 214;
-----DVYNTSNVTKLPPGKDMIGRI 465
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Query Match 3.8%; Score 118.5; DB 1; Length 1612; Best Local Similarity 18.3%; Pred. No. 0.09; Matches 126; Conservative 85; Mismatches 231; Indels 247; Gaps 31; Qy 56 LTQITTENVGQLQLVWARGMOPGKVQVTPLIHDGVMYLANPGDVTQAIDAKTG 108 ::	PRIOR APPLICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/742,128 FILING DATE: 08/09/91 ATTORNEY/AGENT INFORMATION: NAME: Spevack, A. David REGISTRATION NUMBER: 24,743 REFERENCE/DOCKET NUMBER: 75,976 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 295-6759 TELEPHONE: (301) 295-1022 INFORMATION FOR SEG ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1612 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-169-927-2		Db 675 QIRAIDEHTGKVVWSAVLPGGGQANPMTYEANGHQYVAIAGGHHEM 720 Qy 565 STAIGNAVYVFALP 578 : : : Db 721 MTFVSDQLVVYALP 734
	RESULT 6 US-07-642-734C-4 Sequence 4, Application US/07642734C Sequence 4, Application US/07642734C Patent No. 5824513 GENERAL INFORMATION: APPLICANT: Mealpine, J B APPLICANT: Mealpine, J B TITLE OF INVENTION: Recombinant DNA Method for Producing TITLE OF INVENTION: Erythromycin Analogs UNUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS: ADDRESSEE: Edward H. Gorman STREET: Abbott Laboratories D377/AP6D-2 One Abbott STREET: Park Rd CITY: Abbott Park STATE: IL COUNTRY: US ZIP: 60064-1500	286RDTGETVWRHQTLPRDNWDQECTFENMVTNVDVQPSTEMEGLQSINPN	Db 769 YTTDHVESADNTGTLEFVNTDPITVTLNKQGAYFGVLKQVIISGPGNIV 817 Qy 252NLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAV 285 : :: :

amino acid

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US-07-642-734C-4
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APPLICANT:
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                ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                           TITLE OF INVENTION: Method of Directing Biosynthesis of TITLE OF INVENTION: Specific Polyketides NUMBER OF SEQUENCES: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 RGMALYGTNYYFYSWDNHLVALDTATGQYTFDYDR--GQGEDMYSNS-----SGPIV 181
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 VLSTGGGVLFNGGTDRYFRALSQETGETL-WQTRLATVASGQA 530
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COMPUTER: IBM PC compatible
                                                                                       COUNTRY: US
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Abbott Park
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                                                                                                                                                                              E: Steven F. Weinstock
Abbott Laboratories D377/AP6D-2 One Abbott
                                                                                                                                                                                                                                                                                                        Mcalpine, J B
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                  Floppy disk
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US-08-700-651-5

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Sequence 5, Application US/08700651B Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN

APPLICANT: LEECH, JAMES

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US-08-439-009A-4
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 3567 amino acid
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3350 ALRRGGEVVFPLSINRSALRRAEFVPEVLRGMVRAKLRAAGQA 3392
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                                          489 VLSTGGGVLFNGGTDRYFRALSQETGETL-WQTRLATVASGQA 530
                                                                                                                                     453 -----TKLPPGK------------DMIGRIDAIDISTGRTLWSVERAAANYSP 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 40,943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Casuto, Dianne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
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CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
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APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CTYPTOSPOTIGIUM PARVUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
                                                                                1565 KLIDPESGIAIDNSVSGV-FATVPGTAAPKKGGV 1597
                                                                                                                                                              1506 -SYLPFAKNGELIDPISGKYFSGSIAGFISGKAGSQSKSSDESGNPIDPSTNMPYDPKGG 1564
                                                                                                                                                                                                                                                1457 NVLVDPQTGEQIKGSVPYVSLYVKEKNIVTEAAYGL-----PVDPKTGFPIDPI---- 1505
                                                                                                                                                                                                                                                                                                                                     1397 PTNTWWNKISGQTYQVDGKKTILGSAASVIHTALGTPTQTDPTTGLPSDPSTGLPFIPGF 1456
                                                                                                                                                                                                                                                                                                                                                                                                                            1339 DKLQGSHSGTFMPVPGKPQGENGGIMTPEQILEAL--NKLPTSNEVNISPRPSSDAVPDR 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1279 TLVDPSNKKPIPGSHSGFINGTSGEQSHEKDPSTGKPLDPNTGLHPFDEDSGSLINPETG 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1161 THTQYSHTTGHIINP--ETGKVIPGSLPGSLNYPSFHTPQQTDEITGKPVDTVTGLPYDP 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1106 NSTVSGSTSGTTKPKPGIPVNGGGVVPDEEAKDQADK--GKD---GLIVPPTNSINKDPV 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1063 NSTAGIVSGKPGLPPIEDENGNL-FD------PSTNLPIDGNNQLVNPET----- 1105
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                                                                                                                         521 RLATVASGQAISYEVDGMQYVAIAG-----GGV 548
                                                                                                                                                                                                         484 ANYSPVLSTG-----GGVLFNGGTDRYFRA-----LSQETGETLWQT------
                                                                                                                                                                                                                                                                                                            429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 EFLWARDTNY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 DTGEIVWRHQTLPRDN----WDQECTFEMMVTN------VDVQ---PSTEMEGLQS---- 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 GCFVSGHDSAT-----GEELWRNYFIP--RAGEEGDETWGNDYEARWMTGAWGQITYDPV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 THIVHYGSTA--VGPASETQRGTPG------27LYGTNTRFAVRP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 GTNYYFYSWDNHLVALDTATGQYTFDYDRGQGEDMYSNSSGPIVANGYIYAGSTCQYSPF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                979 IDPTTG-LPFNPPTGHLINPTNNNTMDSSFAGAYKYAVSNGIKTDNV------YGLPV 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                            NVCYDMMAVDQ-----EFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVERAA 483
                                                                                                                                                                                                                                                                                                                                                                                   GKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPNIATLNSFGEPTRGMALY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%; Score 114.5; DB 3; Length 1721; 20.2%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------QNMIESIDENGIVTVNE-----DAI--- 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82; Mismatches 227; Indels 245; Gaps
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
SEQUIENCE CHARACTERISTICS:
FENGTH: 1012 amino acids
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GENERAL INFORMATION:
APPLICANT: VAKHAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
478 -----SVERAAANYSPVLSTGGGVLFN--GGTDRYFRALSQETGETLWQTRLATVAS 527
                                      205 VYTVTAADEYQFSSQLIPSGVKTTLFTANIDALTSLSVGGELIFSQVTIHSIEVDVTIYF 264
                                                                                    432 -YDMMAVDQ-EF-----TSMDVYNTSNVTKLPPGKDMI-GRIDAIDISTGRTLW- 477
                                                                                                                              153 DKIGNVLVGEGVTVLSLPTSYDLSYVRLGD-PIPAAGLDP-----KLMATCDSSDRPR 204
                                                                                                                                                                    379 DENGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
                                                                                                                                                                                                                         114 PGGVYALNGTINAVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                     250 VTNLVHYGSTAV------GPAS-----ETQRGTPGGTLYGTNTRF 283
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                                                                                                                                                                                                                                                            325 MEGLQSINP--NAATGERRVLTGVPCKTGTMWQFDAETGEFLWARDTNYQNMIESI---- 378
                                                                                                                                                                                                                                                                                                                                                284 AVRPDTGEIVWRHQTLPRD---NWDQECTFEMMVT------NVDVQPSTE 324
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                                                                                                                                                                                                                                                                                                       61 PGFP--GSVVGAHYTLQSNGSYQFDQ-----MLLTAQNLPVSYNYCRLVSRSLTVRSSTL 113
                                                                                                                                                                                                                                                                                                                                                                                            1 MTNLMDHTQQIVPFIRSLLMPTTGPASIPDDTLEKHTLRSETSTYNLTVGDTGSGLIVFF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 3.7%; Score 113.5; D
Local Similarity 23.0%; Pred. No. 0.12;
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TELEFAX: (703) 413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MENGEL-WHERSAT, STEPHANIE A
MVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
MVENTION: CHIMERIC AND VAC
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55 S. JEFFERSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Mismatches 139; Indels 127; Gaps
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US-09-031-655-10
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 GDPISWTVSGTLAVTIVGG--NYPGALRPVTLVAYERV---AAGSVVTV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 GOAISYEVDGMQYVAIAGGGVSYGSGLN--SALAGERVDSTAIGNAVYV 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 IGFDGTEVTVKAVAIDFGLTTGTNNLVPFNLGGPTSEITQPITSMKLEVVTYKRGGT--A 322
  325 MEGLQSINP--NAATGERRYLTGYPCKTGTMWQFDAETGEFLWARDTNYQNMIESI---- 378
                                                                                   284 AVRPDTGEIVWRHQTLPRD---NWDQECTFEMMVT------
                                                                                                                                                               250 VTNLVHYGSTAV------GPAS------ETQRGTPGGTLYGTNTRF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1755 S. CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 24, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                            61
                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/031,655
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                            PGFP--GSVVGAHYTLQSNGSYQFDQ-----MLLTAQNLPVSYNYCRLVSRSLTVRSSTL 113
                                                                                                                       MTNLMDHTQQIVPFIRSLLMPTTGPASIPDDTLEKHTLRSETSTYNLTVGDTGSGLIVFF 60
                                                                                                                                                                                                        94;
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6017759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                     Infectious bursal disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                             3.7%;
23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24,618
                                                                                                                                                                                                        49; Mismatches 139;
                                                                                                                                                                                                                             Score 113.5; D
Pred. No. 0.12;
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                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                   Length 1012;
                                                                                                                                                                                                              Indels 127;
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                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1026 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
TITLE OF INVENTION: NANOMETER STRUCTURES AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090 TELEFAX: 212-869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 IMMEDIATE SOURCE:
CLONE: p37 ami
                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 PGGVYALNGTINAVT-------FQGSLSEL---TDYSYNGLMSATANIN 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 GDPISWTVSGTLAVTIVGG--NYPGALRPVTLVAYERV---AAGSVVTV 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 -YDMMAVDQ-EF-----TSMDVYNTSNVTKLPPGKDMI-GRIDAIDISTGRTLW- 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 DKIGNVLVGEGVTVLSLPTSYDLSYVRLGD-PIPAAGLDP-----KLMATCDSSDRPR 204
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351 WIMPGTNAALLSVQTQAD------NNNAGD----GQTHIGYNAGGKMNHYFRGTGQ 396
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/542,003 FILING DATE: 13-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
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                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                       TYPE:
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                                     8 WASAGA-LALLAAPAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQITTENVGQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SVERAAANYSPVLSTGGGVLFN--GGTDRYFRALSQETGETLWQTRLATVAS 527
                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                            1026 amino acids
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                                                                              Conservative
                                                                                                                                                                                                                                      Bacteriophage T4
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                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                              protein
                                                                                                 3.6%; Score 112.5; D
20.3%; Pred. No. 0.16;
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                                                                                 74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8471-0005-999
                                                                                                                        DB 2;
                                                                                   281;
                                                                                   Indels 215;
                                                                                                                      Length 1026;
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RESULT 12
US-08-322-760A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 ATVASGQAISYEVDGMQYVAIAGGGVSYGSGLNSALAGERVDSTAIGNAVYVFAL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       947 ----SSYAISYRAGGSN--TNAAGNHSHTFSFGTSSAGDHSHSVGIGAHTHTVAI 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              787 NITGGSGNFANLNSTIESL--KTDIMSSYPIGAPIPWPS----DS----VPAGFALMEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332
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    NAME:
                                           CLASSIFICATION:
                                                                      FILING DATE:
                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSTDLGTKTTSSFDYGTKGTNSTGGHTHSGSGSTSTNGEHSHYIEAWN----GTGVGGNKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAVDQE-FTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVE-----RAAAN 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTLINNGNFRVHYHGGGDNGSTG-PQTADFGWEF-IKNGDFISPRDLIAGKV--RFDRTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDIHSSLRPVRIGLNDGMVGLGRDSFIVDQNNALTTINSNSRINANFRMQLGQSAYIDAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSFGEPTR-----GMALYGTNVYFV---SWDNHLVALDTATGQVTFDVDRGQGED 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQLVWARGMQ--PGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPNIATL 124
                                                                                                                                                                                                                                                      10036
Misrock,
                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                           1155 Avenue of the Americas
                                                                                                                                                                                                                                                                              US
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goldberg, Edward B.
VENTION: MATERIALS FOR THE PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                     Pennie and Edmonds
                                                                 13-OCT-1994
                                           530
                                                                                                                                                                                                                                                                                                                                                                                                                                         NANOMETER STRUCTURES AND USE THEREOF
                                                                                         US/08/322,760A
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; CLONE: p37 amino acid
US-08-322-760A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8471-0003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: 212-869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
                                      523 ATVASGQAISYEVDGMQYVAIAGGGVSYGSGLNSALAGERVDSTAIGNAVYVFAL 577
                                                                                                                                 486 YSPVLST-----
                                                                                                                                                                     836 QTFDKSAYPKLAVAYPSGVIPDMRGQTIKGK-----PSGRAVLSAEADGVKAHSHSASA
                                                                                                                                                                                                                                                                                                                                                731 GTLINNGNFRVHYHGGGDNGSTG-PQTADFGWEF-IKNGDFISPRDLIAGKV--RFDRTG
                                                                                                                                                                                                                                                                                                                                                                                                332
                                                                                                                                                                                                                                                                                                                                                                                                                                  677 CTDAVRPAGAGSFA-----SQNNEDVRAPFYMNIDRTDASAYVPILKQRYVQGNGCYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 ---AVRP-DTGEIVWRHQTLPRDNWDQECTFEMMVTNVDV-----QPSTEMEGLQSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 SITGQVKIGGTANALRIWNAEYGAIFRRSESNFYIIPTNQNEGES-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512 FYAHRKAPTGDETIGRIEAQFAGDVYAKGIIANGNFRVVGSSALAGNVTMSNGLFVQGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 -KFGAPSQVDGTRTIQWNGGTREGQNKNYVIIKAWGNSFNATGDRSRETVFQVSDSQGYY 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125
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                                                                                                                                                                                                                                                                                                       383 IVT-----VNEDAILKELDVEYDVCPTFLGGR--DWPSAALNPDSGIYFIPLNNVCYDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 MVSNSSGP-----GCFVSGHD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212 C. TELEFAX: 66441 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 LQLVWARGMQ---PGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPNIATL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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                                                                                    SSTDLGTKTTSSFDYGTKGTNSTGGHTHSGSGSTSTNGEHSHYIEAWN----GTGVGGNKM
                                                                                                                                                                                                                 MAVDQE-FTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVE-----RAAAN
                                                                                                                                                                                                                                                            NITGGSGNFANLNSTIESL--KTDIMSSYPIGAPIPWPS----DS----VPAGFALMEG
----SSYAISYRAGGSN--TNAAGNHSHTFSFGTSSAGDHSHSVGIGAHTHTVAI 995
                                                                                                                                                                                                                                                                                                                                                                                         NPNAATGERRV------LTGVPCKTGTMWQFDAETGEFLWARDTNYQNMIESIDENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDIHSSLRPVRIGLNDGMVGLGRDSFIVDQNNALTTINSNSRINANFRMQLGQSAYIDAE 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQI--TYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRF---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SATGE-----ELWRN-----YFIPRAGEEGDETWGNDYEARWMTGAW 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSFGEPTR------GMALYGTNVYFV---SWDNHLVALDTATGQVTFDVDRGQGED 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WIMPGTNAALLSVQTQAD-----NNNAGD----GQTHIGYNAGGKMNHYFRGTGQ 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNINTQQGMEINPGILKLVTGSNNVQFYADGTISSIQPI -- KLDNEIFLTKSN--NTAGL 452
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                                                                                                                          -----GGGVLFNGGTDRYFRALSQETGETLWQTRL
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30, Application US/08928361B Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-324-1678 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                483
                                                                                                                                                             428
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                                                                                                                                                                                                                                           385
                                                                                                                                                                                                                                                                                                                         352
                                                                                                                                                                                                                                                                                                                                                                                                     301 IDPTTG-LPFNPPTGHLINPTNNNTMDSSFAGAYKYAVSNGIKTDNV-----YGLPV 351
541 STGEIIDPATKLPIPGSVAGDEILTEVLNITTDEVTGLPIDLETGLPRDPVSGLPQLPNG 600
                                   288 DTGEIVWRHQTLPRDN---WDQECTFEMMVTN-----VDVQ---PSTEMEGLQS----
                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 12-SEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             25 VTPVTDELLANPPAGEWISYGQNQE-----NYRHSPLTQITTENVGQLQLVWARGMQP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                             TNTQYSNTTGNIINP--ETGKVIPGSLPGSLNYPSFNTPQQTDEITGKPVDTVTGLPYDP 540
                                                                                                                                                           NSTVSGSTSGTTKPKPGIPVNGGGVVPDEEAKDQADK--GKD---GLIVPPTNSINKDPV 482
                                                                                                                                                                                                 GCFVSGHDSAT-----GEELWRNYFIP--RAGEEGDETWGNDYEARWMTGAWGQITYDPV 250
                                                                                                                                                                                                                                           NSTAGIVSGKPGLPPIEDENGNL-FD-----PSTNLPIDGNNQLVNPET-----
                                                                                                                                                                                                                                                                               GTNVYFVSWDNHLVALDTATGQVTFDVDRGQGEDMVSNSSGPIVANGVIVAGSTCQYSPF 197
                                                                                                                                                                                                                                                                                                                         GEITGLP-----KDPGSDI-PFNSTTGELV-------DPSTGKPIN 384
                                                                                                                                                                                                                                                                                                                                                           GKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPNIATLNSFGEPTRGMALY 137
                                                                                                                   TNLVHYGSTA--VGPASETQRGTPG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; Mismatches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480.76-1(HV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 108.5; DI Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1043;
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                                                                                                                   GTLYGTNTRFAVRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08928361B Patent No. 6071518 GENERAL INFORMATION:
                                                                                                                 TELEFAX: 650-324-1678 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                     NAME: Verny Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                       FILING DATE: 13-SEP-1996 ATTORNEY/AGENT INFORMATION: NAME: Verny, Hana
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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MOLECULE TYPE:
                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   887 KLIDPESGIAIDNSVSGV-FATVPGTAAPKKGGV 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94306-1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                TOPOLOGY:
                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
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                                                                         1721 amino acids
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                  linear
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5 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                               12-SEP-1997
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THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carolyn
                                                                                                                                                                                                                                                                                                    us 60/026,062
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RESULT 15
US-08-928-361B-11
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                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08928361B Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLIDPESGIAIDNSVSGV-FATVPGTAAPKKGGV 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SYLPFAKNGELIDPISGKYFSGSIAGFISGKAGSQSKSSDESGNPIDPSTNMPYDPKGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVCYDMMAVDQ-----EFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVERAA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STGEIIDPATKLPIPGSVAGDEILTEVLNITTDEVTGLPIDLETGLPRDPVSGLPQLPNG 1278
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                                                                                                         Palo Alto
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                                                                                                                                               PETERS, VERNY, JONES & BIKSA
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                                                                                                                                                                                                          PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
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                                                                                                                            Suite
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
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APPLICATION NUMBER: US 6
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                     482 AAANYSPVLSTG-----GGVLFNGGTDRYFRA-----LSQETGETLWQT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 GKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPNIATLNSFGEPTRGMALY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 VTPVTDELLANPPAGEWISYGQNQE------NYRHSPLTQITTENVGQLQLVWARGMQP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME:
                                                             GFNVLVDPQTGEQIKGSVPYVSLYVKEKNIVTEAAYGL-----PVDPKTGFPIDPI--
                                                                                                                                                                                                                                                                                                                                                                                                                                 AVRPDTGETVWRHQTLPRDN---WDQECTFEMMVTN-----VDVQ---PSTEMEGLQS
                                                                                                                                                                                                                                                                                                                                                                                         PYDPSTGEIIDPATKLPIPGSVAGDEILTEVLNITTDEVTGLPIDLETGLPRDPVSGLPQ 596
                                                                                                   LNNVCYDMMAVDQ-----EFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVER 481
                                                                                                                                           DRPTNTWWNKISGQTFQVDGKKTIPGSAASVIHTALGTPTQTDPTTGLPSDPSTGLPFIP
                                                                                                                                                                                                                           ETGDKLQGSHSGTFMPVPGKPQGENGGIMTPEQ-ILEALNKLPTSNEVNISPRPSSDAVP 715
                                                                                                                                                                                                                                                                     ETGEFLWARDTNYQNMI--ESIDENGIVTVNEDAILKELDV-----EYDVCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDPVTNTQYSNTTGNIINP--ETGKVIPGSLPGSLNYPSFNTPQQTDEITGKPVDTVTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDPVTNLVHYGSTA--VGPASETQRGTPG-------GTLYGTNTRF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STSGSTKPKP-GIPVNGGGVVPDEE-----AKDQADK--GKD---GLIVPPTNSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTNVYFVSWDNHLVALDTATGQVTFDVDRGQGEDMVSNSSGPIVANGVI------VAG
                                                                                                                                                                                     -----TFL--GGRDWPSAAL-----
                                                                                                                                                                                                                                                                                                           LPNGTLVDPSNKKPIPGSHSGFINGTSGEQSHEKDPSTGKPLDPNTGLPFDEDSGSLINP 656
                                                                                                                                                                                                                                                                                                                                               ST---CQYSPFGCFVSGHDSATGEELWRNYFIPRAGEEGDETWGNDYEARWMTGAWGQIT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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36;

- Вb 827 ---SYLPFAKNGELIDPISGKYFSGSIAGFISGKAGSQSKSSDESGNPIDPSTNMPYDPK 883
- Qy
- В

Search completed: August 8, 2001, 19:41:26 Job time: 83 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
Run on:
August 8, 2001, 19:40:03; Search time 19.51 Seconds
(without alignments)
2260.639 Million cell updates/sec

Title:
Perfect score:
3089
Sequence:
Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:
219241
Minimum DB seq length: 200000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

.5 4.3 13055 2 32 4.3 407 2 28 4.1 1365 2	132.5 4.3 13055 2 132 4.3 407 2 128 4.1 1365 2	132.5 4.3 13055 2 132 4.3 407 2 128 4.1 1365 2	132.5 4.3 13055 2 132 4.3 407 2	132.5 4.3 13055 2	132.5 4.3 13055 2	1001	138.5 4.5 424	142 4.6 943 2	110 110 110 110 110 110 110 110 110 110	145 4.7 1645 2	148.5 4.8 668	155.5 5.0 392 2	159.5 5.2 392 2 B8589	167.5 5.4 524 2	167.5 5.4 40/ 2	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	221 5 7.2 221 2 A4137	276.5 9.0 639	313.5 10.1 809 2 A55547	327 10.6 803 2 F83360	340 11.0 808 1 QPKEX	390 12.6 801 1 S00943	392.5 12.7 796 2 H85495	392.5 12.7 796 1 JV0107	439.5 14.2 573 2 S68591	626 2 JQ0706	505 16.3 623 2 B83399	17.7 742 2 JS0326	561 18.2 742 2 A49340	564.5 18.3 738 2 \$14270	18.9 708 2 S5231/		Score Match Length DB ID	Result Query	dP
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ALIGNMENTS

Qy	Qy Db	Qy Db Qy	Que Bes Mat	RESULT S52317 quinoh C; Spec C; Date C; Date C; Accee R; Stoo Eur. J A; Titl A; Refe A; Mole A; Mole A; Resi A; Cros A; Accee A; Statt A; Mole A; Resi A; Cros A; Acce A; Resi A; Cros A; Acce A; Resi A; Cros A; Acce A; Resi A; Resi A; Cros A; Cros A; Cros A; Acce A; Mole C; Gen A; Mole C; Supe
164 VDRGQGEDMVSNSSGPTVANGVTVAGST-CQYSPFGCFVSGHDSATGEELWRNYFIP 219	110 LIWEHRROLPNIATLNSFGE-PTRGMALYGTNVYFVSWDNHLVALDTATGQVTFD 163 : : : : :	3 PTSLIMASAGALALIAAPAFAQVIPVI 1	Query Match 18.9%; Score 583; DB 2; Length 708; Best Local Similarity 27.9%; Pred. No. 1.3e-32; Matches 173; Conservative 95; Mismatches 271; Indels 82; Gaps 22;	RESULT quinohemoprotein ethanol dehydrogenase (EC 1.1.99) type 1 precursor - Comamonas testosteroni C;Species: Comamonas testosteroni C;Species: Comamonas testosteroni C;Date: 08 May-1995 #sequence_revision 21-Jul-1995 #text_change 02-Jun-2000 C;Cates: 582366; 582373; 565908; 552317 C;Date: Storovogel, J; Kraayveld, D.E.; van Sluis, C.A.; Jongejan, J.A.; de Vries, S.; Dui Eur. J. Blochem. 235, 690-698, 1996 Eur. J. Blochem. 235, 690-698, 1996 Eur. J. Blochem. 235, 690-698, 1996 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-708 <5701> A;Residues: 1-708 <5701> A;Residues: 1-708 <5701> A;Residues: 32-64 <5702> A;Rolecule type: protein A;Residues: 32-54 <5702> A;Reference number: 565978 A;Molecule type: protein A;Residues: 32-54 <5702> A;Title: Quinohaemoprotein ethanol dehydrogenase from Comamonas testosteroni. Purific A;Reference number: 565908; MUID:95324580 A;Residues: 32-50, X', 52-54;477-483, X', 485-490 <dej> A;Residues: 32-50, X', 52-54;477-483, X', 485-490 <dej> A;Gene: qhedh C;Keywords: oxidoreductase; quinoprotein ethanol dehydrogenase type 1 #status experimental C;Keywords: oxidoreductase; quinoprotein ethanol dehydrogenase type 1 #status experimental E;132-708/Product: quinohemoprotein ethanol dehydrogenase type 1 #status experimental</dej></dej>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alcohol dehydrogenase, membrane-bound (EC 1.1.-.-) 72K chain precursor - Acetobacter pol c;Species: Acetobacter polyoxogenes A;Variety: strain NBI102B C;Date: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000 C;Accession: S14270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-738 < TAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Tamaki, T.; Fukaya, M.; Takemura, H.; Tayama, K.; Okumura, H.; Kawamura, Y.; Nishiyama Biochim. Biophys. Acta 1088, 292-300, 1991
A;Title: Cloning and sequencing of the gene cluster encoding two subunits of membrane-bc A;Reference number: S14270; MUID:91159482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:D00635; NID:9216185; PIDN:BAA00528.1; PID:9216186
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                                                                                                                                                                                                                                                                                                                            Matches 165;
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                          176
                                                                    137 NIADKGCCDTVNRGAAYWNGKVYFGTFDGRLIALDAKTGKLVWSVNTIPPEAELGKQRSY 196
                                                                                                                          120
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                                                                                                                                                                                        62 ENVGQLQLVWARGMQPGKVQV-TPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLP- 119
                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                         10 SAGALALLAAPAFAQVTPVTDE-----LLANPPAGEWISYGONQENYRHSPLTQITT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 578 -LAARATERQGPG-TVYTFVV 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 GKPQSGTGWNTAKFFNAEPPKSKPFGRLLAWDPVAQKAAWSVEHVSPWNGGTLTTAGNVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 -- AAARDGSKPQDAVPGPYGAHNWHPMSFNPQTGLVYLPAQNVPVNLMDDKKWEFNQAGP 462
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                             --SSGPIVANGVIVAGSTCQYSPFGC--FVSGHDSATGEELWRNYFIPRAGEEGD----
                                                                                                             NIATLNSFGEPTRGMALYGTNVYFVSWDNHLVALDTATGQVTFDVDRGQGEDMVSN---- 175
                                                                                                                                                   SNVGNLKLAWYLDLDTNRGQEGTPLVIDGVMYATTNWSMMKAVDAATGKLLWSYDPRVPG 136
                                                                                                                                                                                                                                   TAGTICAALISGYATMASADDGQGATGEAIIHADDHPGNWMTYGRTYSDQRYSPLDQINR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAIA-GGGVSYGSGLNS 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SMDVYNTSNVTKL-PPGKDMIGRIDAIDISTGRTLWSVERAAANYSPVLSTGGGVL 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQ-EFT----
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                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                       18.3%;
28.0%;
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Pred. No. 2.6e-31;
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                                                                                                                                                                                                                                                                                                                    261;
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310 GIGSNLFLGSIVALKPETGEYVWHFQATPMDQWDYTSVQQIMTLDMPV-------
                                                                                                                                                                                                                                                                                            127
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                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 18.2%;
Local Similarity 28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
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. Bacteriol. 175, 6857-6866, 1993

A;Title: Induction by ethanol of alcohol dehydrogenase activity in Acetobacter pasteu A;Reference number: A49340; MUID:94042848
A;Accession: A49340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Dl3893; NID:g517067; PIDN:BAA40252.1; PID:g452586 C;Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone) C;Keywords: alcohol metabolism; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Acetobacter pasteurianus
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alcohol dehydrogenase (EC 1.1.-.) precursor - Acetobacter pasteurianus (strain C; Species: Acetobacter pasteurianus
                                                                                                                                                                                                                                   203 VAKGLVLIGN--GGSEFGARGFVSAFDAETGKLKWRFYTVPNNKNEPDHAVADNVLMSKA 260
                                                                                                                                                                                                                                                                                                         181 VANGVIVAGSTCQYSPFGC--FVSGHDSATGEELWRNYFIPRAGEEGD-------
                                                                                                                                                                                                                                                                                                                                                                                          143 CDTVNRGAGYWNGKVFWGTFDGRLVAADAKTGKKVWEVNTIPADASLGKQRSYTVDGAVR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 LAWYYTLDTNRGQEATPLVVDGIMYATTNWSKMEALDAATGKLLWQYDPKVPGNIADKGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AGALALLAAPAFAQVTPVTDELL--ANPPAGEWISYGQNQENYRHSPLTQITTENVGQLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 VLMNKAYQTWS-----PTGAWTRQGGGGTVWDSIVYDPVADLYYLGVGNGSPWNYKYR 307
--GTN----TREAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSI 331
                                                                             YKTWGP--KGAWVRQGGGGTVWDSLYYDPVSDLIY---LAVG-----NGSPWNYKYRSE 309
                                                                                                                                                      -ETWGNDYEARWMT----GAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAALPYAAVPARADGQGNTGEAIIHADDHPENWLSYGRTYSEQRYSPLDQINRSNVGDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGEPTRGMALYGTNYYFYSWDNHLVALDTATGQVTFDV-----DRGQGEDMVSNSSGPI- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVWARGMQPGKVQ-VTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLP-NIATLNS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAIAGG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLGLDMNKVGIPDSPEAKQAFVKDLKGWIVAWDPQKQAEAWRVDHKGPWNGGILATGGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DALYTLTGKEWYGIPGDLGGHNFAAMAFSPKTGLVYIPAQQVPFLYTNQVGGFTPHPDSW 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SINPNAATGERRYLTGYPCKTGTMWQFDAETGEFLWARDTNYQNWIESID-ENGIVTVNE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGKGDNLFLGSIVALKPETGEYVWHFQETPMDQWDFTSDQQIMTLDLPI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NGETRHVIVHARKNGFFYIIDAKTGEFISGKNYVYVNWASGLDPKTGRPIYNP 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ETWGNDYEARWMTGA------WGQITYDPVTNLVHYGSTAVGPASETQR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 561; DB 2;
Pred. No. 4.6e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 742;
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357

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alcohol dehydrogenase (EC 1.1...) 72K chain precursor - Acetobacter aceti C;Species: Acetobacter aceti C;Species: Acetobacter aceti C;Date: 31-Mar-1990 #text_change 20-Jun-2000 C;Date: 31-Mar-1990 #text_change 20-Jun-2000 C;Accession: JS0326 C;Accession: JS0326 R;Inoue, T.; Sunagawa, M.; Mori, A.; Imai, C.; Fukuda, M.; Takagi, M.; Yano, J. Bacteriol. 171, 3115-3122, 1989
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C;Keywords: alcohol metabolism; NAD; oxidoreductase
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-742/Product: alcohol dehydrogenase 72K dehydrogenase chain #status predicted <ADC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:D90004; GB:M26951; NID:g216193; PIDN:BAA14058.1; PID:g216194 A;Experimental source: strain K6033 A;Note: amino terminal of mature protein is confirmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-742 <INO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Cloning and sequencing of the gene encoding the 72-kilodalton dehydrogenase sub A;Reference number: JS0326; MUID:89255070 A;Accession: JS0326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            591
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                                               278 --GTN----TREAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSI 331
  310 GIGSNLFLGSIVALKPETGEYVWHFQATPMDQWDYTSVQQIMTLDMPVK-----
                                                                                                   261 YKTWGP--KGAWVRQGGGGTVWDSLVYDPVSDLIY---LAVG-----NGSPWNYKYRSE
                                                                                                                                                                                                                                                    181 VANGVIVAGSTCQYSPFGC--FVSGHDSATGEELWRNYFIPRAGEEGD------
                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AGALALLAAPAFAQVTPVTDELL--ANPPAGEWISYGQNQENYRHSPLTQITTENVGQLQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCY------DMMA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NGEMRHVIWHAP-KNGFFYVLDAKTGEFLAGKNYVYQNWANGLDPLTGRPIYNPD 411
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                                                                                                                                                                                                                                                                                                      CDTVNRGAGYWNGKVFWGTFDGRLVAADAKTGKKVWAVNTIPADASLGKQRSYTVDGAVR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVWARGMQPGKVQ-VTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLP-NIATLNS 126
                                                                                                                                                                                                     VAKGLVLIGN--GGAEFGARGFVSAFDAETGKLKWRFYTVPNNKNEPDHAASDNILMNKA 260
                                                                                                                                                                                                                                                                                                                                                     FGEPTRGMALYGTNVYFVSWDNHLVALDTATGQV-----TFDVDRGQGEDMVSNSSGPI- 180
                                                                                                                                                                                                                                                                                                                                                                                                    LLGYYTLDTNRGQEATPLVVDGIMYATTNWSKMEALDAATGKLLWQYDPKVPGNIADKGC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAALPYAAVPARADGOGNTGEAIIHADDHPENWLSYGRTYSEQRYSPLDQINRSNVGDLK 82
                                                                                                                                                -ETWGNDYEARWAT----GAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.7%; Score 547.5; DB 2 27.8%; Pred. No. 3.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97; Mismatches 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 115;
             358
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             80
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                                                                                                                                                                                                                                                              182 HGAGYTM---TGAPTIVKDGKTGKVLLIHGSS--GDEFGVVGRLFARDPDTGEEIWMRPFV
                                                                                                                                                                                                                                                                                                              166 RGQGEDMVSNSSGPIVANG-----VIVAGSTCQYSPFGCF--VSGHDSATGEELWRNYFI 218
                                                                                                                                                                                                                                                                                                                                                                  128
                                                                                                                                                                                                                                                                                                                                                                                                       114 HRRQLPN----IATLNSFGEPTRGMALYGTNVYFVSWIDNHLVALDTATGQVTFD-;-VD 165
          312 MMVTNVDVQPSTEMEGLQSINPN-----AATGERRVLTGVPCKTGTMW--QFDAETGEFL 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PTSLLWASAGALAL---LAAPAFAQVTPVTDELLAN--PPAGEWISYGQNQENYRHSPLT 57
                                                                                                                                                                                                            PR-----AGEEGDETWGNDYEA-----RWMTGA---WGQITYDPVTNLVHYG 257
                                                                                                                                                                                                                                                                                                                                                                  YNHRLPDDIRPCCDVVN-----RGAAIYGDKVFFGTLDASVVALNKNTGKVVWKKKFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVNADNVFKLTPAWSYSFGDEKQRGQ-ESQAIVSDGVIYVTASYSRLFALDAKTGKRLWT 127
                                                            AGNPGPWNTWARTAKGGNPHDYDSLY-TSGQVGVDPSSGEVKWFYQHTPNDAWDFSGNNE
                                                                                                           STAVGPASETQRGTPGG-----TLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QITTENVGQLQLVWARGM----QPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGLLRPSLHCLAFAVALGSAGAALAKDVTWEDIANDDKTTGDVLQYGMGTHAQRWSPLK 68
                                                                                                                                                                EGHMGRLNGKDSTVTGDVKAPSWPDDRNSPTGKVESWSHGGGAPWQSASFDAETNTIIVG
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Conservative

105;

Mismatches

Indels

Gaps

181

237

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quinoprotein alcohol dehydrogenase PA1982 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83399 C;Accession: B83399 C;Rictover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warremer, P.; Hickey, M.J.; R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warremer, P.; Hickey, M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                   adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                            A;Cross-references: GB:AE004624; GB:AE004091; NID:g9947973; PIDN:AAG05370.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-623 <STO>
                                                                                                                                                                                                                                                                                    A; Reference number: A82950; A; Accession: B83399
                                                                                                                                                                                                                                                                                                                                   A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A; Reference number: A82950; MUID: 20437337
A; Gene: exaA; PA1982
                                                                                                                                                                                                                                     A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            523 ILATGGDLLFQGLANGEFHAYDATNGSDLYKFDAQSGIIAPPMTYSVNGKQYVAVEVGWG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 KPHADSWNVGLDMTKNGLPDTPE-ARTAYIKDLHGWLLAWDPVKMETVWKIDHKGPWNGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 GIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 NPNAATGE-RRVLTGVPCKTGTMWQFDAETGEFLWARDTNYQNMIESID-----EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 GIYPISMGGVGRTSGWTVNHSYIAAFSLDGKA 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 VLSTGGGVLFNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----DMMAVDQEFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVERAAANYSP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GEMRHVIVHAP-KNGFFYVLDAKTGEFLSGKNYVYQNWANGLDPLTGRPMYNPD 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IAGGGVSYGSGL---NSALAGERVDSTA 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYTLNG-----KFWYGI-PGPLGAHNEMAMAYSPKTHLVYIPAHQIPFGYKNQVGGF 463
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A;Gene: moxF
C;Keywords: a
F;1-27/Domain
F;28-626/Prodi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alcohol dehydrogenase (acceptor) (EC 1.1.99.8) alpha chain precursor - Methylobacterium N.Alternate names: methanol dehydrogenase 62K large chain C; Species: Methylobacterium extorquens C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Oct-1999 C; Accession: JQ0706; S07908 R; Anderson, D.J.; Morris, C.J.; Nunn, D.N.; Anthony, C.; Lidstrom, M.E. Gene 90, 173-176, 1990 G; C.J.; Nunn, D.N.; Anthony, C.; Lidstrom, M.E. A; Title: Nucleotide sequence of the Methylobacterium extorquens AM1 moxF and moxJ genes A; Reference number: JQ0706; MUID:90337342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M31108; NID:g150017; PIDN:AAA25380.1; PID:g150018 A;Experimental source: strain AM1 R;Nunn, D.N.; Day, D.; Anthony, C. Biochem. J. 260, 857-862, 1989 A;Title: The second subunit of methanol dehydrogenase of Methylobacterium A;Reference number: S04644; MUID:89350892 A;Accession: S07908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 28-50,'XX',53 <NUN>
A;Residues: 28-50,'XX',53 <NUN>
A;Note: the source is designated as Methylobacterium extorquens
C;Comment: This enzyme oxidizes methanol to formaldehyde.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-626 < AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Keywords: alcohol metabolism; oxidoreductase
;1-27/Domain: signal sequence #status predicted <SIG>
;28-626/Product: alcohol dehydrogenase (acceptor) #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics
                    186 TIAPYVVKDKVIIGSSGAELGVRGYLTAYDVKTGEQVWRAYATGPDKDLLLASDFNIKNP
                                                                                                                               126 RAVACCDLVNRGLAYWPGDGKTPALILKTQLDGNVAALNAETGETVWKVENSDIKVGSTL 185
                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                        10 SAGALALLA-AP-AFAQVTPVTDELLANPPAGE-WISYGQNQENYRHSPLTQITTENVGQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 485 NYSPVLSTGGGVLFNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAIA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414 --RPVEREGQRPPLPEPG------QKHGKAVEVSPPFLGGKNWNPMAYSQDTGLFY 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 VPANHWKEDYWTEEVSYTKGSAYLGMGFRIKRMYDDHVGSLRAMDPVSGKVVWEHKEHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 LVLFDYKAKDGKIVKATAHADRNGFFYVVDRSNGKLQNAFPFVDNITWASHIDLKTG---
                                                                                                                                                                                                                                                                                                                                                                      7
                                                                        ATLNSFGEPTRGMALYGTN-----VYFVSWDNHLVALDTATGQVTFDVDRGQGEDMVSN 175
                                                                                                                                                                                                                                                                                             LQLVW--ARGMQPGKVQVTPLIHDGVMYL--ANPGDVIQAIDAKTGDLIWEHR-RQLPNI 121
                                                                                                                                                                                                                                                                                                                                                    SVSALAMLALAPAALSSGAYANDKLVELSKSDDNWVMPGKNYDSNNFSDLKQINKGNVKQ 66
                                                                                                                                                                                                                                         LRPAWTFSTGLLNGH-EGAPLVVDGKMYIHTSFPNNTFALGLDDPGTILWQDKPKQNPAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VGYG-GAVPLWGGDMADLTRPVAQGGSFWVFKLP 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGVSYGSGLNSALAGERVDST---AIGNAVYVFALP 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LWAGVLATAGNLVFTGTGDGYFKAFDAKSGKELWKFQTGSGIVSPPITWEQDGEQYLGVT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPLNNVCYDMMAVDQEFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVERAAA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WARDTNYQNMIESIDENGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYF 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.2%; Score 468.5; DB 2; 25.4%; Pred. No. 9.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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A;Residues: 1-573 <XIA>
A;Cross-references: EMBL:U41040; NID:g1127819; PIDN:AAA83765.1; PID:g1127820
A;Note: the authors did not translate the codons for residues 1-2
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                      δÃ
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A;Accession: $68591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methanol dehydrogenase (EC 1.1.1.244) heavy chain - Methylophilus methylotrophus (str C;Species: Methylophilus methylotrophus A;Variety: strain W3A1 C;Date: 06-Dec_1996 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: S68591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
247 KLNLFYYGSGNPAPWNETMR--PGDNKWTMTIWGRDL-----DTGMAKWGYQKTPHDEW
                                                250 VTNLVHYGSTAVGPASETQRGTPGG-----TLYGTNTRFAVRPDTGEIVWRHQTLPRDNW
                                                                                                                                                                                                                                                          153 LDTATGQVTFDVDRGQGEDMVSNSSGPIVANGVIVAGSTCQYSPFGC--FVSGHDSATGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        522 YLKARDSDTGDLLWKFKIPSGAIGYPMTYTHKGTQYVAIYYGVGGWPGVGLVFDLADPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 AGEWISYGQNQENYRHSPLTQITTENVGQLQLVW--ARGMQPGKVQVTPLIHDGVMYL-- 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 LKELD-VEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQEFTSMDVYNTS 450
                                                                                                                                                                                                                                                                                                                                                              94 ANPGDVIQAIDAKTGDLIWEHR-RQLPNIATLNSFGEPTRGMALYGTNVYFVSWDNHLVA 152
                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 NKW-TMTIFGRDADTGEAKFGYQKTPHDEWD------YAGVNVMMLSEQKD------ 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 TLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSINPN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 HYGQKGLGTGTWEGD---AWKIGGGTNWGWYAYDPGTNLIYFGTGNPAPWNETMR--PGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 RAGEE--GDETWGNDYEARWMTGA---WGQITYDPVTNLVHYGSTAVGPASETQRGTPGG 274
                                                                                                                                                                                                          LDAKTGKINWEVEVCDPKVGSTLTQAPFVAKDTVLMG--CSGAELGVRGAVNAFDLKTGE
                                                                                                                                                                                                                                                                                                              AFPNNTYALNLNDPGKIVWQHKPKQDASTKAVMCCDVVDRGLAYGAGQIVKKQANGHLLA
                                                                                                                                                                                                                                                                                                                                                                                                                 AGAWPIATGGYYSQHNSPLAQINKSNVKNVKAAWSFSTGVLNGH-EGAPLVIGDMMYVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAI---AGGGVSYG------S 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLGAVGAFKKLANYTQMGGGVVVFSL 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLNSALAGERY-DSTAIGNAVYVFAL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLNMYPGPKGDRQNYEGLGQIKAYNAITGDYKWEKMERFAVWGGTMATAGDLVFYGTLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTRMDHLAKDICPSAMGYHNQGHDSYDPKRELFFMGINHICMDWEPFMLPYRAGQFFVGA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGERRVLTGVPCKTGTMWQFDAETGEFLWAR----DTNYQNMIESIDENGIVTVNEDAI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVTKLPPGK-----DMIGRIDAIDISTGRTLWSVERAAANYSPVLSTGGGVLFNGGTDR 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KDGKARKLLTHPDRNGIVYTLDRTDGALVSANKLDDT--VNVFKSVDLKTGQPVRDPEY 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.2%;
                                                                                                                                                       -NYFIPRAGE-:-EGDETWGNDYEARWMTGA---WGQITYDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 439.5; DB Pred. No. 8.4e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
  298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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C;Date: 30-Jun-1992 #sequence_revision 12-Dec-1997 #text_change 16-Jun-2000 C;Accession: D64735; JV0107; A45997; S45201; I41228 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucose dehydrogenase (pyrroloquinoline-quinone) (EC 1.1.99.17) - Escherichia C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: strain K12
R;Yamada, M.; Sumi, K.; Matsushita, K.; Adachi, O.; Yamada, Y.
R;Yamada, M.; Sumi, K.; Matsushita, K.; Adachi, O.; Yamada, Y.
3. Biol. Chem. 268, 12812-12817, 1993
A;Title: Topological analysis of quinoprotein glucose dehydrogenase in Escherichia coli A;Reference number: A45997; MUID:93286127
A;Accession: A45997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE000122; GB:U00096; NID:g1786315; PIDN:AAC73235.1; PID:g1786316; A;Experimental source: strain K-12, substrain MG1655 R;Cleton-Jansen, A.M.; Goosen, N.; Fayet, O.; van de Putte, P. J. Bacteriol. 172, 6308-6315, 1990 J. Bacteriol. 172, 6308-6315, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: D64735
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                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-796 <FUJ>
A;Cross-references: EMBL:D26562; NID:g473770; PIDN:BAA05580.1; PID:g473791
A;Experimental source: strain K-12 substrain W3110
R;Yamada, M.; Asaoka, S.; Saier, M.H.; Yamada, Y.
J. Bacteriol. 175, 568-571, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-58,'L',60-148,'H',150,'KRRCHT',157-192,'K',194-796 <CLE>
A;Cross-references: GB:X51323; NID:g41553; PIDN:CAA35706.1; PID:g41554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Cloning, mapping, and sequencing of the gene encoding Escherichia coli quinoproa;Reference number: JV0107; MUID:91035240
A;Accession: JV0107
                                                                                                                                                                                  A;Title: Characterization of the gcd gene from Escherichia coli K-12 W3110 and regulatia;Reference number: I41228; MUID:93123180
A;Accession: I41228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S45181
A; Accession: S45201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-20 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-796 <BLAT>
A;Molecule type: DNA
A;Residues: 1-148,'H',150,'KRRCHT',157-192,'K',194-665,'H',667-796 <RES>
A;Cross-references: GB:D12651; NID:g216555; PIDN:BAA02174.1; PID:g216556
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, January 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Fujita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 QYI-----GSMYGVGGWPGVGLVFDLTDPSAGLGAVGAFRELQNHTQMGGGLMVFSL 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 QYVAIAGGGVSYGSG------LNSALAG-----ERVDSTAIGNAVYVFAL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 VERAAANYSPVLSTGGGVLFNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGM 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 VAEKVDPAVNVFKKVDLKTGTPVRDPEFATRMDHKGTNICPSAMGFHNQGVDSYDPESRT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 DQECTFEMMVTNVDVQPSTEMEGLQSINPNAATGERRVLTGVPCKTGTMWQFDAETGEFL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 KWEKFAAWGGTLYTKGGLVWYATLDGYLKALDNKDGKELWNFKMPSGGIGSPMTYSFKGK 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFIPLNNVCYDMMAVDQEFTSMDVYNTSNVTKLP----PGKDMIGRIDAIDISTGRTLWS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYAGLNHICMDWEPFMLPYRAGQFFVGATLAMYPGPNGPTKKEMGQIRAFDLTTGKAKWT 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WARDIN-YOMMIESIDENGIVTVNEDAILKELDVE-YDVCPTFLGGRDWPSAALNPDSGI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFAGVNQMVLTD------QPVN-----GKMTPLLSHIDRNGILYTLNRENGNLI 341
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780

---TKMGDYIVAYALP 792

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F;120-140/Domain: transmembrane *status predicted <TM5>
F;93,95/Binding site: ubiquinone (Arg, Asp) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;63-81/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Pathway: respiratory chain
C;Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
C;Superfamily: glucose dehydrogenase (pyrroloquinone; respiratory chain; transmembran C;Reywords: oxidoreductase; pyrroloquinoline quinone; respiratory chain; transmembrane #status predicted <TM1>
F;11-37/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: catalyzes the oxidation of D-glucose to D-gluconic acid by ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: gcd
A; Map position: 3 min
C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;96-110/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;41-59/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
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                                                                                                                                                                                                                                                                                          419
                                                                                                                                                                                                                                                                                                                                    572 FTPPSEQGTLVFPGNLGMFEWGGISVDPNREVAIANPMALPFVSKLIPRGPGNPMEQPKD
                                                                                                                                                                                                                                                                                                                                                                                   401
                                                                                                                                                                                                                                                                                                                                                                                                                              512 PEKPVPQGAAKGDYVTPTQPFSELSFRPTKDLSGADMWGATMFDQLVCRVMFHQMRYEGI 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 DTATGQV--TF-------DVDRGQGEDMVSNSSGPTVANGVIV-AGS-TCQYS- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 INADNYHNLKEAWVFRTGDVKQPNDPGEITNEVTPIKVGDTLYLCTAHQRLFALDAASGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 LTWAGFNDPQEINGTLSADATPAEA-ISPVADQ-----DWPAYGRNQEGQRFSPLKQ 185
                                                                                                                                           673 SALDLKTNEVVWKKRIGTPQDSMPFPMPVPVPFNMGMPMLGGPISTAGNVLFIAATADNY
                                                                                                                                                                                                                                          632 AKGTGTESGIQPQYGVPYGVTLN------PFLS------PFGLPCKQPAWGYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 12.7%; Score 392.5; DE Local Similarity 24.3%; Pred. No. 2.4e-1
    563 VDSTAIGNAVYVFALP 578
                                                    733 LRAYNMSNGEKLWQGRLP--AGGQATPMTYEVNGKQYVVISAGGHGSFG-
                                                                                                                                                                                           466 DAIDISTGRTLWSVERAAANYS------PV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LLWAS-----AGALALLAAPAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTFEMMVTNVDVQPSTEMEGLQSINPNAATGERRVLTGVPCKTGTMWQFDAETGEFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RETSGVIRGEDVNTGELLWA--FDPGAKDPNAIPSDEHTETENS-----PNSWAPAAY 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAENGKLCETFANKGYLNLQSNMPDTKPG----LYEPTSPPIITDKTIVMAGSYTDNFST 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKWHYD----PELKTNESFQHVTCRGVSYHEAKAETASPEVMADCPRRIILPVNDGRLIAI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITTENVGQLQLVWA------RGMQPGKV--QVTPLIHDGVMYLANPGDVIQAIDAKTGD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAKLDLYYLPMGVTTPDIWGGNRTPEQERYASSI-LALNATTGKLAWSYQTVHHDLWDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PFGCFVSGHDSATGEELWRNYFIPRA-----GEEGDETWGNDYEARWMTGAWGQITY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIWEHRRQLPNIATLNSFGEPT-RGMALYGTNVYFVS--
                                                                                              FRALSQETGETLWQTRLATVASGQA--ISYEVDGMQYVAI-AGGGVSYGSGLNSALAGER 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LPAQPT-----LADITVN----GQKVPVIYAPAKTGNIFVLDRRNGELVVPA
                                                                                                                                                                                                                                                                                          -----DSGI-----YFIPLNNVCYDMMAVDQEFTSMDVYNTSNVTKLPPGKDMIGRI
                                                                                                                                                                                                                                                                                                                                                                                 -----VCPTFLGGRDWPSAALNP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----WARDTNYQNMIESIDENGI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 231; Indels 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VTVNEDAILKEL--DVEYD-- 400
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                                                                                                                                                                                                ----LSTGGGVLFNGGT-DRY 505
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C; Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: H85495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucose dehydrogenase [imported] - Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Date: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: H85495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J. iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-796 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone;
733 LRAYNMSNGEKLWQGRLP--AGGQATPMTYEVNGKQYVVISAGGHGSFG----
                                   506 FRALSQETGETLWQTRLATVASGQA--ISYEVDGMQYVAI-AGGGVSYGSGLNSALAGER 562
                                                                                                                                                                                                                                                                                                                                                                                                                   469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 LTWAGFNDPQEINGTLSADATPAEA-ISPVADQ------DWPAYGRNQEGQRFSPLKQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 EKWHYD----PELKTNESFQHVTCRGVSYHEAKAETASPEVMADCPRRIILPVNDGRLIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 LIWEHRRQLPNIATLNSFGEPT-RGMALYGTNVYFVS-------WDNHLVAL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LLWAS-----AGALALLAAPAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQ 58
                                                                           SALDLKTNEVVWKKRIGTPQDSMPFPMPVPVPFNMGMPMLGGPISTAGNVLFIAATADNY 732
                                                                                                                     DAIDISTGRTLWSVERAAANYS------PV------LSTGGGVLFNGGT-DRY 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTFEMMVTNVDVQPSTEMEGLQSINPNAATGERRVLTGVPCKTGTMWQFDAETGEFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAKLDLYYLPMGYTTPDIWGGNRTPEQERYASSI-LALNATTGKLAWSYQTVHHDLWDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RETSGVIRGFDVNTGELLWA--FDPGAKDPNAIPSDEHTFTFNS-----PNSWAPAAY
                                                                                                                                                             AKGTGTESGIQPQYGVPYGVTLN-------PFLS-----PFGLPCKQPAWGYI 672
                                                                                                                                                                                                     ------DSGI-----YFIPLNNVCYDMMAVDQEFTSMDVYNTSNVTKLPPGKDMIGRI 465
                                                                                                                                                                                                                                             FTPPSEQGTLVFPGNLGMFEWGGISVDPNREVAIANPMALPFVSKLIPRGPGNPMEQPKD 631
                                                                                                                                                                                                                                                                                                                           PEKPVPQGAAKGDYVTPTQPFSELSFRPTKDLSGADMWGATMFDQLVCRVMFHQMRYEGI 571
                                                                                                                                                                                                                                                                                                                                                                       ----WARDINYQNMIESIDENGI--
                                                                                                                                                                                                                                                                                                                                                                                                           -----LPAQPT-----LADITVN---GQKVPVIYAPAKTGNIFVLDRRNGELVVPA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAENGKLCETFANKGVLNLQSNMPDTKPG----LYEPTSPPIITDKTIVMAGSVTDNFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTATGQV--TF------DVDRGQGEDMVSNSSGPIVANGVIV-AGS-TCQYS- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITTENVGQLQLVWA-----RGMQPGKV--QVTPLIHDGVMYLANPGDVIQAIDAKTGD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PFGCFVSGHDSATGEELWRNYFIPRA-----GEEGDETWGNDYEARWMTGAWGQITY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INADNVHNLKEAWVFRTGDVKQPNDPGEITNEVTPIKVGDTLYLCTAHQRLFALDAASGK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                       -----VCPTFLGGRDWPSAALNP---
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                     2.4e-19;
ches 231;
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A; Residues: 1-801 <CLE>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       563 VDSTAIGNAVYVFALP 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TKMGDYIVAYALP 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169;
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F;39-57/Domain: transmembrane #status predicted <TM2>
F;61-79/Domain: transmembrane #status predicted <TM3>
F;94-108/Domain: transmembrane #status predicted <TM4>
F;118-137/Domain: transmembrane #status predicted <TM4>
F;118-137/Domain: transmembrane #status predicted <TM5>
F;91,93/Binding site: ubiquinone (Arg, Asp) #status predicted
F;471/Active site: Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
C;Keywords: oxidoreductase; pyrroloquinoline quinone; respiratory chain; transmembrane
F;9-35/Domain: transmembrane #status prodicted F;9-35/Domain: transmembrane #status prodicted cmpo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Nucleotide sequence of the gene coding for quinoprotein glucose dehydrogenas A;Reference number: S00943; MUID:88289368
A;Accession: S00943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: catalyzes the oxidation of D-glucose to D-gluconic acid by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain LMD 79.41 C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S00943
R; Cleton-Jansen, A.M.; Goosen, N.; Odle, G.; van de Putte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Pathway: respiratory chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucose dehydrogenase (pyrroloquinoline-quinone) (EC 1.1.99.17) - Acinetobacter calco C; Species: Acinetobacter calcoaceticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X07235; NID:g38711; PIDN:CAA30222.1; PID:g38712
                                                                  538 SKTQPFSDLNLAPQDKLTDKDMWGATMLDQLMCRVSFKRLNYDGIYTPPSENGTL----
390 AILKELDVEYDVCPTFLGGRDWPSAALNPDS----
                                                                                                                                                                                                                                                                                      314 VTNVDVQPSTEMEGLQSINP--NAATGERRVLTGVP------CKTG--TMWQFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 EPT-RGMALYGTN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 PETAQAVPGVAE-----SDWPAYGRTQAGVRYSPLKQINDQNVKDLKVAWT--LRTGD 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 PAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQITTENVGQLQLVWARGMQPGK 79
                                                                                                                                                                                                               LADIKNKAGQTVPAIYVLTKTGNAFVLDRR---NGQPIVPVTEKPVPQTVKRGPQTKGEFY
                                                                                                                                                                                                                                                                                                                                                            -----GTP--DIWGGDRTELKERYANSMLAINASTGKLVWNFQTTHHDLWDMDVPSQPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLLW--VFDTGAADPNAMPGEGTTFVHNS----PNAWAPLAYDAKLDIV-YVPTGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EELWRNYFIPRAGE-----EGDETWGNDYEARWMTGAWGQITYDPVTNLVHYGSTAVGP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QNGQVNLQEFMPYAYPGGYNPTSPGIVTGSTVVIAGSVTDNYSNKEPSG-VIRGYDVNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLTCRGVMYYDANNTTEFATSLQSKKSSSTQCPRKVFVPVNDGRLVAVNADTGKACTDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                  ASETQRGTPGGTLYG-----TNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMM 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKTDNDSGETTNQVTPIKIGNNMFICTAHQQLIAIDPATGKEKW---RFDPKLKTDKSFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V------QVTPLIHDGYMYLANPGDVIQAIDAKTGDLIWEHRRQLPNIATLNSFG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88;
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Pred. No. 3.7e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- VYFVSWDNHLVALDTATGQVTFDVD
                                                                                                                                         RDTNYQNMIESIDENGIVTVNED
GIYFI ---
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   425
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glucose dehydrogenase (pyrroloquinoline-quinone) (EC 1.1.99.17) - Gluconobacter oxydans C;Species: Gluconobacter oxydans C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-May-1998 C;Accession: S17716; S19265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Pathway: respiratory chain
C;Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
C;Keywords: oxidoreductase; pyrroloquinoline quinone; respiratory chain; transmembrane
E;9-28/Domain: transmembrane #status predicted <TM1>
F;35-54/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Cleton-Jansen, A.M.; Dekker, S.; van de Putte, P.; Goosen, N. Mol. Gen. Genet. 229, 206-212, 1991
A;Title: A single amino acid substitution changes the substrate specificity of quinoprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-808 <CLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;35-54/Domain: transmembrane #status predicted <TM2>F;60-76/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: X62710; NID: g58416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S19265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S19265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: X62710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S17716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S17716; MUID:92017653
δõ
                                          Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: catalyzes the oxidation of D-glucose to D-gluconic acid by ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    122-138/Domain: transmembrane #status predicted <TM5>
91,93/Binding site: ubiquinone (Arg, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94-110/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 692 KKRIGTIRDSLPNLFQLPAVKIGVPGLGGSISTAGNVMFVGATQDNYLRAFNVTNGKKLW 751
                                                                                                                                                                                                                             128
                                                                                                                                     188 TNVSNLKVAWHIHTKDMMNSNDPGEQTNEATPIEFNNTLYMCSLHQKLFAVDGATGNVKW 247
                                             248 VYDPKLQINPGFQHLTCRGVSFHETPANAMDSDGNPAPTDCAKDSILPVN-DGRLVEVDA 306
                                                                                        113 EHRRQL---PNIATLN----SFGE-PTRGMALYGT-----NVYFVSWDNHLVALDT 155
                                                                                                                                                                                                                                                                        13 ALALLAAPAFAQVTPVTDELLA-------NPPAGEWISYGQNQENYRHSPLTQITT 61
                                                                                                                                                                                62 ENVGQLQLVW------ARGMQPGKV--QVTPLIHDGVMYLANPGDVIQAIDAKTGDLIW 112
                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLP--AGGQATPMTYEINGKQYVVIMAGGHGSFG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTRLATVASGQA--ISYEVDGMQYVAI-AGGGVSYGSGLNSALAGERVDSTAIGNAVYVF 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTEQGVQPMYGVPY-----GVEISAFLSPLGLPCKQPAWGYVAGVDLKTHEVVW 691
                                                                                                                                                                                                                             AVLALFASLFTDPHDISGELPTQIANASPADPDNVPASEWHAYGRTQAGDRWSPLNQINA 187
                                                                                                                                                                                                                                                                                                                        159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-212, 'A', 214-808 <GOO>
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---VFPGNLGVFEWGGMSVNPDRQVAVMNPIGLPFVSRLIPADPNRAQTAKG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                      Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                             11.0%;
21.8%;
                                                                                                                                                                                                                                                                                                                        98; Mismatches
                                                                                                                                                                                                                                                                                                                                             Score 340; DB 1;
Pred. No. 1.1e-15;
       -SSGPIVANGVIVA----
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                                                                                                                                                                                                                                                                                                                                                                   Length 808;
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    ---GSTCQYSP 196
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A;Reference number: A82950;
A;Accession: F83360
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                               QУ
                                                                            В
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A; Residues: 1-803 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                             Query Match
                                                                                                                                                                      Matches
                                                                                                                                                                                          Best Local Similarity
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glucose dehydrogenase PA2290 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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R; Stover, C.K.; Pham, X.Q.; Adman, S.; Yuan, Y.; Brody, Adman, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE004654; GB:AE004091; NID:g9948311; PIDN:AAG05578.1; A;Experimental source: strain PAO1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                              A;Gene: gcd; PA2290
C;Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 DTGKTCSGFGNNGEIDLRVPNQPYTTPGQYEPTSPPVITDKLIIANSAITDNGSVKQASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    571 LRYEGPFTPPSLKGSLIFPGDLGMFEWGGLAVDPQRQVAFANPISLPFVSQLVPRGPGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         514 VPAPETPVPQGAAPGDHTSPTQPMSQ---LTLRPKNPLNDSDIWGGTIFDQMFCSIYFHT
                                                                                  103 LLWLPWFRRPLLADGPAPLGTAALGVAVVLAGAAAVGSQ-FTNPGQIVGRIDRDSGMTST 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                751 LTTGKVLWQDRLPAGAQATPITYAINGKQYI-----VTYAGGHNSF-----PTRMGD
                              37 ----PAGEWISYGQNQENYRHSPLTQITTENVGQLQLVWARGMQPGKV-------Q 81
                                                                                                                                             6 LLW------ASAGALALLAAPAFAQVTPVTDELLANP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVYIPMGV-----GTPDQWGGDRTKDSERFAPGIVALNADTGKLAWFYQTVHHDLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of Pseudomonas aeruginosa PA01, an 50; MUID:20437337
                                                                                                                                                                                                                                         10.6%;
21.9%;
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84;
                                                                                                                                                                                                                                         Score 327; DB 2;
Pred. No. 8.6e-15;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                             265;
                                                                                                                                                                                                                                                                 Length 803;
                                                                                                                                                                                                             Indels 244;
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A;Gene: quiA C;Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone) C;Keywords: membrane protein; oxidoreductase
                                                                                                                                                                                                                                                                                                           A; Title: The pca-pob supraoperonic cluster A; Reference number: A5547; MUID:95095936 A; Accession: A55547
                                                                                                                                                                                                                                                                                                                                                            quinate-shikimate dehydrogenase (EC 1.1.99.-) - Acinetobacter calcoaceticus C;Species: Acinetobacter calcoaceticus C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999 C;Accession: A55547 R;Elsemore, D.A.; Ornston, L.N. J. Bacteriol. 176, 7659-7666, 1994
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                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-809 <ELS>
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A55547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                778 LIVAGGHGSFG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        720 MGGSITTAGGVAFLSGTLDQYLRAYDVKDGKQLWQARLP--AGGQATPMSYTGKDGRQYV 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 PYAVIMHPEMSPIGLPCQAPSWGDVAGIDLTTAKVVWQHKNGTSRDNTPVPIGLTVGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 CPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQEFT---SMDVYNTSNVTK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    556 LRPPLTERDMWGSSPFDQMLCRIQFRSLRYEGQYTPPSEQGSL-----I
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                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 NTPLKVNGMLYACTAHSKVLALDPDTGAEIWRFDPQIQSPVGFKGFAHMTCRGVSYYDEE
3 PTSLLWASAGALALLAA-PAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSINP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRGQGE----DMVSNSSGPIVANGVIVAG----STCQYSPFGCFVSGHDSATGEELWRNY 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----EFLWA------RDTNYQNMIESIDENGIVTVNEDAILKELDVEYDV 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSGNPDETEPLAPGKFY-TRNSPNMWSLASVDEKLGQVY---LPLGNQMPDQWGGNRTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIPRAGEEGDETWGNDYEARWMTGAWGQITYDPVTNLVHYGSTAVGPASETQRG---TPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYARSDVGAPPAALSEAGKAVAASCPRRLFLPTADARLIAINADNGKVCEDFGVKGAVDL
                                                160;
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                                                               Similarity
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LPPGKDMIGRIDAIDISTGRTLWSVERAAA-NYSPV------
                                                                 10.1%;
                                          ; 08
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                                        Pred. No. 7.5e
0; Mismatches
                                                               Score 313.5; DB 2
Pred. No. 7.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TRMGDYIIAYALPR
                                                                                                                                                                                                                                                                                                                                               of Acinetobacter calcoaceticus contains
                                                                                  DB 2;
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                                            Indels
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                                          26;
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F;1-33/Domain: signal sequence #status predicted <SIG>
F;49-53/Region: gene C-binding
F;294-497/Domain: pyrroloquinoline quinone-binding #status predicted <PQB>
                                                                                                                                                   A:Cross-references: DDBJ:D50670; NID:g1502278; PIDN:BAA09321.1; PID:d1009963; PID:g15 A;Experimental source: strain VM15C C:Comment: This enzyme is a membrane-bound enzyme. It oxidizes low molecular weight s
                                                                                                                                                                                                                                                                                                                                                                                                      polyvinyl-alcohol dehydrogenase (acceptor) (EC 1.1.99.23) precursor - Pseud N;Alternate names: PvA dehydrogenase C;Species: Pseudomonas sp. C;Date: 10-Sep-1996 #sequence_revision 18-Oct-1996 #text_change 08-Oct-1999 C;Accession: JC4881
                                                                                A;Gene: pdh C;Keywords: alcohol metabolism; oxidoreductase
                                                                                                                                      C; Genetics
                                                                                                                                                                                                                                                                                 A;Reference number: JC4881; MUID:96376165
A;Accession: JC4881
                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-639 <SHI>
                                                                                                                                                                                                                                                                                                                             A; Title: Cloning and characterization of the gene encoding
                                                                                                                                                                                                                                                                                                                                                    R;Shimao, M.; Tamogami, T.; Nishi, K.; Harayama, S. Biosci. Biotechnol. Biochem. 60, 1056-1062, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             585 GLYTAPGTDVSLSFPGSLGGMNWGSIAFDPTHRYMFVNDMRLGLWIQLIKQTPEDIKIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525 VIEQPIKVADIPGEQYSKTQPRSVEMPQIGNQTLKESDMWGATPFDQLMCRINFKSMRYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QYSPF----GCFVSGHDSATGEELWRNYFIPRAGEEGDETWGNDYEARWMTGAWGQITYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWDNHLVALDTATG------QVTFDVDRGQGEDMVSN----SSGPIVANGVIVAGSTC 192
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                                                                                                                                                                                                                                                                                                                             pyrroloquinoline
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RESULT 15
A41378
C;Species: Paracoccus denitrificans (fragment)
C;Species: Paracoccus denitrificans
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 08-Oct-1999
C;Accession: A41378
       밁
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                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-221 <RAS>
                                                                                                                                                                                                                                                                                                     A;Title: Isolation, sequencing, and mutagenesis of the gene encoding cytochrome c-553i A;Reference number: A41378; MUID:92041583
A;Accession: A41378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
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VCPAALGTKDQQPAAFSPKTNLFYVPTNHVCMDYEPFRVAYTAGQPYVGATLSMYPAPNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QMWG-----PAGGSIWSAPTIDPKRGLVYVATSNSYTEVHHEGSDAV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDFALGNSPILHTLQDGRQYIVVGQKSGAVYAMDPDNDGELIWMR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPISSG----NEAFATNDQWECCKFRGALVALDALSGKVLWKTYTTQKEPAPFRLNKLGK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQLPAGAPAQYA--IFFSDWTKAAVALDAQTGKQLWKTTIDDQPGVQMTGSPTYHEGKLF 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGEPTRGMALYGTNVYFVSWDNHLVALDTATG----QVTFDVDRG-----QGEDM 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPNIATLNS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWGPPSASMPLDGPKCKGKIPPID--LSTP--DQWNGWGAGITNARFQPNPGLTAADVPR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.2%; Score 221.5; DB 2; llarity 30.1%; Pred. No. 2.8e-08; Conservative 34; Mismatches 86;
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                                                                                                                                     Length 221;
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Search completed: August 8, 2001, 19:40:33 Job time: 30 sec

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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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AFSK_STROO
AFSK_STROO
YZZ3_METJA
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PLMN_PIG
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Query Match Best Local Similarity

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Score 569; DB 1; Pred. No. 2.8e-32;

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1894; CAA58066.1; 1480; CAA70688.1; 1PRO00345; 1PRO01479; 1PRO012372; 11PRO02372; 11PRO02373; 10PRO02363; BACTERIA PS00364; BACTERIA PS003655; BACTERIA PS003655; BACTERIA PS003655; BACTERIA PS003655; BACTERIA PS003655; BACTERIA PS003655; BACTER	SWISS-PROT entry is copyright. It is the Swiss Institute of Bioinfor uropean Bioinformatics Institute. By non-profit institutions as lonited and this statement is not removies requires a license agreement (Sund an email to license@isb-sib.ch).	FROM N.A. SS11 / DSM 616 A.K.; (NOV-1996) t WTIC ACTIVITY ED ACCEPTOR. TOR: PQO AND IIT: HETEROTET IET HETEROTET LER UNKNOWN SU EX (BY SIMILA LLULAR LOCATI (POTENTIAL).	1998 (Rel. 37, 1998 (Rel. 37, 1999 (Rel. 38, DEHYDROGENASE ICTER EUROPAEUS. A; PROTEODACTER CCETODACTER. IXID=33995;	•	S S S S S S S S S S S S S S S S S S S
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Kawamura Y., Nishiyama M., Horinouchi S., Beppu T.;
"Cloning and sequencing of the gene cluster encoding two subunits of
membrane-bound alcohol dehydrogenase from Acetobacter polyoxogenes.";
Biochim. Biophys. Acta 1088:292-300(1991).

-!- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: METHANOL).

-!- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE +
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01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ALCOHOL DEHYDROGENASE [ACCEPTOR] PRECURSOR (EC 1.1.99.8).
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COFACTOR: PQQ AND HEME.
SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROM
SUBUNIT: HETEROTETRAMER) THAT FORMS THE ALCOHOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01011; Bacterial_PQQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                         389
                                                                                                                                                                                                                                                                             308
                                                                                                                                                                                                                                                                                                               270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                  197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        send an email to license@isb-sib.ch).
LFQGLANGEFHAYDATNGSDLFHFAADSGIIAPPVTYLANGKQYVAVEVG
                                                                NLGLDMNKVGIPDSPEAKQAFVKDLKGWIVAWDPQKQAEAWRVDHKGPWNGGILATGGDL
                              LFNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAIAGG 546
                                                                                                                                                                   DAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQEFT-SMDVY
                                                                                                                                                                                                                                                                                                          GTPGGTLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQ
                                                                                                                                                                                                                                                                                                                                              VLMNKAYQTWS----PTGAWTRQGGGGTVWDSIVYDPVADLVYLGVGNGSPWNYKYR
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                                                                                               NTS---NVTKLPPG-----KDMIGRIDAIDISTGRTLWSVERAAANYSPVLSTGGGV 496
                                                                                                                                   DALYTLTGKEWYGIPGDLGGHNFAAMAFSPKTGLVYIPAQQVPFLYTNQVGGFTPHPDSW
                                                                                                                                                                                                                                        SINPNAATGERRVLTGVPCKTGTMWQFDAETGEFLWARDTNYQNMIESID-ENGIVTVNE
                                                                                                                                                                                                                                                                          SEGKGDNLFLGSIVALKPETGEYVWHFQETPMDQWDFTSDQQIMTLDLPI------
                                                                                                                                                                                                                                                                                                                                                                             -----ETWGNDYEARWMTGA------WGQITYDPVTNLVHYGSTAVGPASETQR
                                                                                                                                                                                                                                                                                                                                                                                                               TVDGAPRIAKGRVIIGN--GGSEFGARGFVSAFDAETGKVDWRFFTVPNPKNEPDAASDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIADKGCCDTVNRGAAYWNGKVYFGTFDGRLIALDAKTGKLVWSVNTIPPEAELGKQRSY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIATLNSFGEPTRGMALYGTNVYFVSWDNHLVALDTATGQVTFDVDRGQGEDMVSN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNVGNLKLAWYLDLDTNRGQEGTPLVIDGVMYATTNWSMMKAVDAATGKLLWSYDPRVPG
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Pro; IPR000345;
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PS00190; CYTOCHROME_C; 1.
uctase: POO: Norm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01011; Bacterial_PQQ; 6.
PS00363; BACTERIAL_PQQ_1;
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                                                                                                                                                                                                       NGETRHVIVHARKNGFFYIIDAKTGEFISGKNYVYVNWASGLDPKTGRPIYNP
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28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 564.5; DB 1
Pred. No. 5.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEME (COVALENT) (BY SIMILARITY).
HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
1E2B6ED7ECD92AF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

ALCOHOL DEHYDROGENASE [ACCEPTOR]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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01-NOV-1997
15-JUL-1999
                                                                                                                                                               BINDING
BINDING
METAL
SEQUENCE
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SUBUNIT I).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression in Acetobacter pasteurianus.";
Appl. Environ. Microbiol. 63:1131-1138(1997).
-i- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: METHANOL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of the genes encoding the three-component membrane-bound alcohol dehydrogenase from Gluconobacter suboxydans and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=IFO 12528; MEDLINE=97208225; PubMed=9055427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gluconobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gluconobacter suboxydans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     005542;
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                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                                                               Pfam; PF01011; Bacterial_POQ; 6.
PROSITE; PS00363; BACTERIAL_POQ_1; 1.
PROSITE; PS00364; BACTERIAL_POQ_2; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no war
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE
                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                     Oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000345; -.
                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P38539; 4AAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kondo K., Horinouchi
                                                                                                                                                                                                                                                                                                                                                              InterPro;
 62
                               16
                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADHS), THAT FORMS THE ALCOHOL DEHYDROGENASE COMPLEX. SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: PQQ AND HEME. SUBUNIT: HETEROTRIMER (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPACE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REDUCED ACCEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
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                                                          LWASAGALALLAA--PAFAQV---TPVTDELLANPPAGEWISYGQNQENYRHSPLTQITT 61
 ENVGQLQLVWARGMQPGKVQV-TPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLP- 119
                               LLSCAAALAFSAAVPVAFAQEDTGTAITSSDNGGHP-GDWLSYGRSYSEQRYSPLDQINT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997 (Rel. 35, Created)
1997 (Rel. 35, Last sequence update)
1999 (Rel. 38, Last annotation update)
DEHYDROGENASE [ACCEPTOR] PRECURSOR (EC 1.1.99.8)
                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                            IPR002372;
                                                                                                                                                                                                                                                                                                                                                                              IPR001479;
                                                                                        17.9%; ilarity 27.4%; Conservative 9.
                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                                                     PQQ;
                                                                                                                                                               342 B
653 H
656 H
657 I
82968 MW;
                                                                                                                                                                                                                                                                                       Heme;
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                                                                                        ; Score 553.5; DB 1; Pred. No. 3.5e-31; 97; Mismatches 255
                                                                                                                                                                                                                                                                                     Periplasmic; Membrane; Signal.
                                                                                                                                                             ALCOHOL DEHYDROGENASE [ACCEPTOR].

PYRROLIDONE CARBOXYLIC ACID.

BASE (POTENTIAL).

HEME (COVALENT) (BY SIMILARITY).

HEME (COVALENT) (BY SIMILARITY).

IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

1RON (HEME AXIAL LIGAND) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subdivision;
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                                                                                                                      DB 1;
                                                                                           255;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ALCOHOL DEBYDROGENASE [ACCEPTOR] PRECURSOR (EC ADHA OR ADH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHET_AC
P18278;
                                                                                                            [2]
3D-STRUCTURE MODELING.
MEDLINE-95289964; PubMed-7772016;
Cozier G.E., Giles I.G., Anthony (
                                                                                                                                                                                                         "Cloning and sequencing of the gene encoding the 72-kilodalton dehydrogenase subunit of alcohol dehydrogenase from Acetobacter
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=89255070; PubMed=2722742;
                             Biochem. J. 308:375-379(1995).
-!- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR -
                                                                                                                                                                                           aceti
                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
                                                                                                                                                                                                                                                                                                                                                                            Acetobacter aceti
-
                                                                           "The structure of the quinoprotein alcohol dehydrogenase of acetobacter aceti modelled on that of methanol dehydrogenase
                                                                                                                                                                                                                                           Yano K.;
                                                                                                                                                                                                                                                          Inoue
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=435;
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                                                             Methylobacterium extorquens.
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                                                                                                                                                                          Bacteriol. 171:3115-3122(1989).
COFACTOR: PQQ AND HEME
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                 REDUCED ACCEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTL-WSVERAANYS------PVL 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGE-RRVLTGVPCKTGTMWQFDAETGEFLWARDTNYQNMIESIDE-NGIVTVNEDAILK 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSINPNA 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _ACEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAGNVIFQGLANGEFHAYDATNGNDLYSFPAQSAIIAPPVTYTANGKQYVAVEVGWGGI 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGGGVLFNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAI-----
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                                                                                                                                                                                                                                                          T., Sunagawa M., Mori A., Imai C., Fukuda M., Takagi M.,
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                                                                                                              Anthony C.;
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464 KPHADSWNVGLDMTKNGLPDTPE-ARTAYIKDLHGWLLAWDPVKMETVWKIDHKGPWNGG
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                                                                                                                                                                                                  GIGSNLFLGSIVALKPETGEYVWHFQATPMDQWDYTSVQQIMTLDMPVK----
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SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
                                ----DMMAVDQEFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVERAAANYSP 488
                                                                                                  GIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCY-----
                                                                                                                                                                                                                                                                    YKTWGP--KGAWVRQGGGGTVWDSLVYDPVSDLIY---LAVG-----NGSPWNYKYRSE
                                                                                                                                                                   NPNAATGE-RRVLTGVPCKTGTMWQFDAETGEFLWARDTNYQNMIESID-----EN
                                                                                                                                                                                                                                   --GTN----TRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSI 331
                                                                                                                                                                                                                                                                                                                                   VAKGLVLIGN--GGAEFGARGFVSAFDAETGKLKWRFYTVPNNKNEPDHAASDNILMNKA
                                                                                                                                                                                                                                                                                                                                                                    VANGVIVAGSTCQYSPFGC--FVSGHDSATGEELWRNYFIPRAGEEGD------
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                                                                                                                                                                                                                                                                                                   -ETWGNDYEARWMT----GAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVWARGMQPGKVQ-VTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLP-NIATLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAALPYAAVPARADGQGNTGEAIIHADDHPENWLSYGRTYSEQRYSPLDQINRSNVGDLK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLGYYTLDTNRGQEATPLVVDGIMYATTNWSKMEALDAATGKLLWQYDPKVPGNIADKGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00363; BACTERIAL_PQQ_1; 1.
PS00364; BACTERIAL_PQQ_2; 1.
PS00190; CYTCCHROME_C; 1.
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                                                                                                                                  GEMRHVIVHAP-KNGFFYVLDAKTGEFLSGKNYVYQNWANGLDPLTGRPMYNPD
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649
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                                                                 -KFWYGI-PGPLGAHNFMAMAYSPKTHLVYIPAHQIPFGYKNQVGGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 547.5; DB 1
Pred. No. 8.8e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9C6C9268DABB825A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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(COVALENT) (BY SIMILARITY).
(HEME AXIAL LIGAND) (BY SIMILARITY).
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RESULT 5
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Q9Z4J7;
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30-MAY-2000 (
01-0CT-2000 (
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                       "X-ray structure of the quinoprotein ethanol dehydrogenase from Pseudomonas aeruginosa: basis of substrate specificity."; J. Mol. Biol. 297:961-974(2000).
-i- FUNCTION: OXIDIZE PRIMARY ALCOHOLS AND ALSO ACTS ON SECONDARY ALCOHOL, BUT NOT HIGHLY ACTIVE ON METHANOL.
                                                                                                                                                                                                                                                                                                                                                                          Schobert M., Goerisch H.;

"Cytochrome c550 is an essential component of the quinoprotein ethanol "Cytochrome c550 is an essential component of the quinoprotein ethanol oxidation system in Pseudomonas aeruginosa: cloning and sequencing of oxidation system in Pseudomonas aeruginosa: an addacont anotalidahude
                                                             -!- SUBUNIT: HOMODIMER.
-!- SUBCELULAR LOCATION: PERIPLASMIC.
-!- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Wathrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                       -1- COFACTOR: PQQ AND CALCIUM
                                                                                                                                                                                                                                                    verter
                                                                                                                                                                                                                                                                 MEDLINE=20202376; PubMed=10736230;
                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 35-616
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-52 FROM N.A. STRAIN-ATCC 17933;
                                                                                                                                                                                                                                    Goerisch H.;
                                                                                                                                                                                                                                                                                                                                      Microbiology
                                                                                                                                                                                                                                                                                                                                                        dehydrogenase."
                                                                                                                                                                                                                                                                                                                                                                    the genes encoding cytochrome c550
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99173751; PubMed=10075429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99041560; PubMed=9826187;
Diehl A., Wintzingerode F., Goerisch H.;
"Quinoprotein ethanol dehydrogenase of Pseudomonas aeruginosa is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-ATCC 17933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homodimer: sequence of the gene and deduced structural properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QUINOPROTEIN
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                                                                                                                                                                                                                                                Diehl A., Knaute T.,
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 Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
ETHANOL DEHYDROGENASE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma subdivision; Pseudomonadaceae;
 Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                             Stezowski J.J., Hoehne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE004624; AAG05370.1; -. EMBL; AF068264; AAC79657.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 DHM1_PARDE P12293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1FLG; 30-AUG-00.
InterPro; IPR002372;
                                                                                                                                                                                          485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRRQLPN----IATLNSFGEPTRGMALYGTNVYFVSWDNHLVALDTATGQVTFD---VD 165
                                                                                                                                                                                                                                                                                    --RPVEREGORPPLPEPG------QKHGKAVEVSPPFLGGKNWNPMAYSQDTGLFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVNADNVFKLTPAWSYSFGDEKQRGQ-ESQAIVSDGVIYVTASYSRLFALDAKTGKRLWT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QITTENVGQLQLVWARGM----QPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGLLRPSLHCLAFAVALGSAGAALAKDVTWEDIANDDKTTGDVLQYGMGTHAQRWSPLK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTSLLWASAGALAL - - - LAAPAFAQVTPVTDELLAN - - PPAGEWISYGQNQENYRHSPLT
                                                                                             ---VGYG-GAVPLWGGDMADLTRPVAQGGSFWVFKLP
                                                                                                                           GGGVSYGSGLNSALAGERVDST---AIGNAVYVFALP 578
                                                                                                                                                          {\tt LWAGVLATAGNLVFTGTGDGYFKAFDAKSGKELWKFQTGSGIVSPPITWEQDGEQYLGVT}
                                                                                                                                                                                      NYSPVLSTGGGVLFNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAIA 544
                                                                                                                                                                                                                         VPANHWKEDYWTEEVSYTKGSAYLGMGFRIKRMYDDHVGSLRAMDPVSGKVVWEHKEHLP
                                                                                                                                                                                                                                                   IPLNNVCYDMMAVDQEFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVERAAA 484
                                                                                                                                                                                                                                                                                                                    WARDTNYQNMIESIDENGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYF 424
                                                                                                                                                                                                                                                                                                                                                   LVLFDYKAKDGKIVKATAHADRNGFFYVVDRSNGKLQNAFPFVDNITWASHIDLKTG---
                                                                                                                                                                                                                                                                                                                                                                             MMYTNVDVQPSTEMEGLQSINPN----AATGERRVLTGVPCKTGTMW--QFDAETGEFL
                                                                                                                                                                                                                                                                                                                                                                                                              AGNPGPWNTWARTAKGGNPHDYDSLY-TSGQVGVDPSSGEVKWFYQHTPNDAWDFSGNNE
                                                                                                                                                                                                                                                                                                                                                                                                                                            STAVGPASETQRGTPGG-----TLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGHMGRLNGKDSTVTGDVKAPSWPDDRNSPTGKVESWSHGGGAPWQSASFDAETNTIIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR-------AGEEGDETWGNDYEA-----RWMTGA----WGQITYDPVTNLVHYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGAGYTM--TGAPTIVKDGKTGKVLLIHGSS--GDEFGVVGRLFARDPDTGEEIWMRPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGQGEDMVSNSSGPIVANG-----VIVAGSTCQYSPFGCF--VSGHDSATGEELWRNYFI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YNHRLPDDIRPCCDVVN-----RGAAIYGDKVFFGTLDASVVALNKNTGKVVWKKKFAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ009858; CAA08896.1; -.
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139
623
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                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 505; DB 1;
Pred. No. 6.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUINOPROTEIN ETHANOL DEHYDROGENASE
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32DDE5DF20B291D6 CRC64;
                   631 AA
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                                                                                                 614
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harms N., de Vries G.E., Maurer K., Hoogendijk J., Stouthamer A.H.; "Isolation and nucleotide sequence of the methanol dehydrogenase structural gene from Paracoccus denitrificans."; J. Bacteriol. 169:3969-3975(1987).

-i- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR - ALDEHYDE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
METHANOL DEHYDROGENASE SUBUNIT 1 PRECURSOR (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE-87307969; PubMed-3114231; Harms N., de Vries G.E., Maurer K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPHA SUBUNIT) (MEDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pfam; PF01011; Bacterial_PQQ; 7.
pr0SITE; PS00363; BACTERIAL_PQQ_1; 1.
pr0SITE; PS00364; BACTERIAL_PQQ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paracoccus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paracoccus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001479; InterPro; IPR002372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P38539; 4AAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M17339; AAA88366.1;
                                                                                                                                                                                                                                                                                                                           Local
                               219
                                                              185
                                                                                             170
                                                                                                                                                                                       66
                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: PERIPLASMIC.

MISCELLANEOUS: MDH IS THE MAJOR PROTEIN IN THE CELL DURING GROWTH ON METHANOL (IN P.DENITRIFICANS MDH CONSTITUTES UP TO 15% OF THE TOTAL CELL PROTEIN).

SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: PQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REDUCED ACCEPTOR.
                                                                                                                                                                                                                 TENVGQLQLVW--ARGMQPGKVQVTPLIHDGVMYLANP-GDVIQAIDA-KTGDLIWEHR-
 FNAPNPHYGQKNLGLETWEGD----AWKIGGGTNWGWYAYDPEVDLFYYGSGNPAPWNETM
                                                                                                                                                                                                                                                                                TSLLWASAGALALL-AAPAFAQVTPVTDEL--LANPPAGEWISYGQNQENYRHSPLTQIT
                                                            KVGSTLTIAPYVIKDLVLVGSSGAELGVRGYVTAYDVKSGEMRWRAFATGPDEELLLAED
                                                                                           EDMVSNSSGPIVANGVIVAGSTCQYSPFGCFVSGHDSATGEELWRNYFI------
                                                                                                                        KQNPTARTVACCDVVNRGLAYWPGDDQVKPLIFRTQLDGHIVAMDAETGETRWIMENSDI 184
                                                                                                                                                        RQLPNIATLNSFGEPTRGMALYGTN------VYFVSWDNHLVALDTATGQVTFDVDRGQG
                                                                                                                                                                                       KENVKQLRPAWSFSTGVLHGH-EGTPLVVGDRMFIHTPFPNTTFALDLNEPGKILWQNKP
                                                                                                                                                                                                                                                   SSLAMAVAMGLAVLTTAPATA - - - - - NDQLVELAKDPA - NWVMTGRDYNAQNYSEMTDIN
                                                                                                                                                                                                                                                                                                                 166;
                                                                                                                                                                                                                                                                                                                              Similarity
                             --PRAGEE--GDETWGNDYEARWMTGA---WGQITYDPVTNLVHYGSTAVGPASETQ
                                                                                                                                                                                                                                                                                                                                                                                         135
418
335
631 /
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                                                                                                                                                                                                                                                                                                                Conservative 111;
                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQQ;
                                                                                                                                                                                                                                                                                                                                                                                                         69799 MW;
                                                                                                                                                                                                                                                                                                                              16.0%;
                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                 Score 495; DB 1;
Pred. No. 3.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                            ASE (POTENTIAL).
0934DC93FFC5730B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subdivision;
                                                                                                                                                                                                                                                                                                                Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1.99.8) (MDH LARGE
                                                                                                                                                                                                                                                                                                                                             Length 631;
                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                   Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group;
                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT
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PIR: A413/o,
PIR: A413/o,
PIR: A413/o,
PIR: A913/o,
PIR: A413/o,
PIR: A413/o,
PAH: POBLICATION
PIR: A113/o,
P
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _PARDE
                                                                                                                                                                                              EMBL; U34346; AAC44555.1; -. EMBL; M75583; AAA25574.1; -. EMBL; M75583; A41378.
                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the mutant strain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation, sequencing, and mutagenesis of the cytochrome c553i of Paracoccus denitrificans are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stouthamer A.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92041583; PubMed=1657873; Ras J., Reijnders W.N.M., van Spa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-ARR-1993 (Rel. 25, Created)
Ol-CTT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE DEHYDROGENASE XOXF PRECURSOR (EC 1.1.99.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 173:6971-6979(1991). COFACTOR: PQQ (BY SIMILARITY).
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DHMI_METOR STANDAM.

ID DHMI_METOR STANDAM.

AC P15279;
DT 01-APR-1990 (Rel. 14, Created)
DT 00-APR-1990 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

T 15-DEC-1998 (Rel. 37, Last annotation update)

"""HANOL DEHYDROGENASE SUBUNIT 1 PRECURSOR (EC 1
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SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN-ATCC 27886; MEDLINE-89008094; PubMed-2459109; Machlin S.M., Hanson R.S.; "Nucleotide sequence and transcripti
                                                                                                                        Methylobacterium organophilum XX
Bacteria; Proteobacteria; alpha
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SEQUENCE
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DCA996F1BCC5A3CE CRC64;
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gene.";
J. Bacteriol. 170:4739-4747(1988).
- i- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
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SUBUNIT: THE HOLDENZYME MDH HAS AN ALPHA-2/BETA-2 CONFIGURATION
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                                                                                                                                                                                                                                 NAATGERRVLTGVPCKTGTMWQFDAETGEFLWAR---DTNYQNMIESIDENGIVTVNEDA
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SNVTKLPPGK-----DMIGRIDAIDISTGRTLWSVERAAANYSPVLSTGGGVLFNGGTD
                                                         YGTRMDHLAKDVCPSAMGYHNQGHDSYDPKRELFFMGINHICMDWEPFMLPYRAGQFFVG
                                                                                                                ILKELD-VEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQEFTSMDVYNT
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BY SIMILARITY.
BY SIMILARITY.
BASE (POTENTIAL).
8768F6B8371E5DFF CRC64;
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Pred. No. 5.
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15-JUL-1999 (Rel. 38, Last annotation update)
METHANOL DEHYDROGENASE SUBUNIT 1 PRECURSOR (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson D.J., Morris C.J., Nunn D.N., Anthony C., Lidst "Nucleotide sequence of the Methylobacterium extorquens moxJ genes involved in methanol oxidation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1990 (Rel.
01-APR-1990 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methylobacterium extorquens.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Methylobacterium group; Methylobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P16027;
            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                 Ghosh M., Anthony C., Harlos K., Goodwin M.G., Blake C.; "The refined structure of the quinoprotein methanol dehydrogenase from Methylobacterium extorquens at 1.94 A."; Structure 3:177-187(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Blake C.C.F., Ghosh M., Harlos K., Avezoux A., Anthony C.;
"The active site of methanol dehydrogenase contains a disulphide bridge between adjacent cysteine residues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      extorquens AM1
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MEDLINE=89350892; PubMed=2504152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-AM1
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                                                                                                                                                                                         -i- SUBGULTI: THE HOLOENZYME MDH HAS AN ALPHA-2/BETA-2 CONFIGURATION OF A LARGE ALPHA AND A SMALL BETA SUBUNIT.
-i- SUBCELLULAR LOCATION: PERIPLASMIC, BUT ASSOCIATED WITH INNER
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                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                 -!- COFACTOR: PQQ.
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95253818; PubMed=7735834;
                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.94 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95384759; PubMed=7656012;
                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY:
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                                                                                                                                                                              MEMBRANE.
                                                                                                                                                                                                                                                                   REDUCED ACCEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Struct. Biol. 1:102-105(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   second subunit of methanol dehydrogenase
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PROSITE; PS00363; BACTERIAL_PQQ_1;
PROSITE; PS00364; BACTERIAL_PQQ_2;
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PIR; S07908; S07908.
PIR; J00706; J00706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRPAWTFSTGLLNGH-EGAPLVVDGKMYIHTSFPNNTFALGLDDPGTILWQDKPKQNPAA
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                                                            STANDARD;
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J. Biol. Chem. 267:22289-22297(1992).
-i- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR -
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PROSITE; PS00363; BACTERIAL_PQQ_
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InterPro; IPR001479; -
InterPro; IPR002372; -
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MEDLINE=94059969; PubMed=8241148;
White S., Boyd G., Mathews F.S., Xia Z.-X., Dai W.-W., Zhang Y.-F.
Davidson V.L.;
"The active site structure of the calcium-containing quinoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xia Z.-X., Da
Mathews F.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 32:12955-12958(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methylophilus methylotrophus (Bacterium W3A1).
Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Last annotation update)
METHANOL DEHYDROGENASE SUBUNIT 1 (EC 1.1.99.8) (MDH LARGE ALPHA
SUBUNIT) (MEDH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF A LARGE ALPHA AND A SMALL BETA SUBUNIT.
SUBCELLULAR LOCATION: PERIPLASMIC, BUT ASSOCIATED WITH INNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PER TETRAMER.
SUBUNIT: THE
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Best Local S
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P1897;
01-APR-1990 (Rel. 14, Created)
01-NOV-1997 (Rel. 35, Last seque
01-OCT-2000 (Rel. 40, Last annot
GLUCOSE DEHYDROGENASE [PYRROLOQU
                                                                         Cleton-Jansen A.-M., Goosen N., Fayet O., van de Putte "Cloning, mapping, and sequencing of the gene encoding coli quinoprotein glucose dehydrogenase."; J. Bacteriol. 172:6308-6315(1990).
                                                                                                                                                                                                          Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                        Bacteria; P
Escherichia
                                 SEQUENCE FROM N.A. STRAIN-K12 / W3110;
MEDLINE=93123180; PubMed=8419307; Yamada M., Asaoka S., Saier M.H.
                                                                                                                                   MEDLINE=91035240; PubMed=2228962;
                                                                                                                                                STRAIN-K12;
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Last annotation update)
[PYRROLOQUINOLINE-QUINONE] (EC 1.1.99.17).
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Pred. No. 3.5e-23;
)9; Mismatches 254;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
    DOMAIN
                                                                                                                                                                                                                                                       EMBL; X51323; CAA35706.1; -. EMBL; D12651; BAA02174.1; -. EMBL; D26562; CAB20298.1; -. EMBL; AE000122; AAC73235.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: D-GLUCOSE + ACCEPTOR = + REDUCED ACCEPTOR.
-!- COFACTOR: PQQ.
                   TRANSMEM
                                    DOMAIN
                                                 TRANSMEM
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                                                                                                               Oxidoreductase;
                                                                                                                                              Pfam; PF01011; Bacterial_PQQ; PROSITE; PS00363; BACTERIAL P
                                                                                                                                                                                           EcoGene; EG10369; gcd.
InterPro; IPR001479; -.
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HSSP; P38539; 4AAH.
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                                                                                                                                   PROSITE;
                                                                                                                                                                                InterPro;
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TOPOLOGY.

MEDLINE=93286127; PubMed=8509415;

MEDLINE=93286127; PubMed=8509415;

Matsushita K., Adachi O., Yamada Y.;

Vamada M., Sumi K., Matsushita K., Adachi O., Yamada Y.;

Vamada M., Sumi K., Matsushita K., Adachi O., Yamada Y.;

Vamada M., Sumi K., Matsushita K., Adachi O., Yamada Y.;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure of the quinoprotein glucose dehydrogenase of Escherichia coli modelled on that of methanol dehydrogenase from Methylobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Systematic sequencing of the Escherichia coli genome: analysis of the 2.4-4.1 min (110,917-193,643 bp) region."; Nucleic Acids Res. 22:1637-1639(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of the gcd gene from Escherichia coli K-12 W3110 and regulation of its expression.";
J. Bacteriol. 175:568-571(1993).
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                                                                                                          PS00363; BACTERIAL_PQQ_1; 1.
PS00364; BACTERIAL_PQQ_2; 1.
uctase; PQQ; Transmembrane; Inner membrane;
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                                                                                                                                                                                                             FRALSQETGETLWQTRLATVASGQA--ISYEVDGMQYVAI-AGGGVSYGSGLNSALAGER
                                                                                                                                 VDSTAIGNAVYVFALP 578
                                                                              ---TKMGDYIVAYALP
                                                                                                                                                                                                                                                                                                                                              DAIDISTGRTLWSVERAAANYS-----PV----LSTGGGVLFNGGT-DRY
                                                                                                                                                                                                                                                                                                                                                                                                AKGTGTESGIQPQYGVPYGVTLN------PFLS-----PFGLPCKQPAWGYI
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                                                                                                                                                                                   LRAYNMSNGEKLWQGRLP--AGGQATPMTYEVNGKQYVVISAGGHGSFG-
                                                                                                                                                                                                                                                                                        SALDLKTNEVVWKKRIGTPQDSMPFPMPVPVPFNMGMPMLGGPISTAGNVLFIAATADNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTPPSEQGTLVFPGNLGMFEWGGISVDPNREVAIANPMALPFVSKLIPRGPGNPMEQPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEKPVPQGAAKGDYVTPTQPFSELSFRPTKDLSGADMWGATMFDQLVCRVMFHQMRYEGI 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAKLDLYYLPMGYTTPDIWGGNRTPEQERYASSI-LALNATTGKLAWSYQTVHHDLWDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RETSGVIRGFDVNTGELLWA--FDPGAKDPNAIPSDEHTFTFNS-----PNSWAPAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAENGKLCETFANKGVLNLQSNMPDTKPG----LYEPTSPPIITDKTIVMAGSVTDNFST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKWHYD---PELKTNESFQHYTCRGVSYHEAKAETASPEVMADCPRRIILPVNDGRLIAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PFGCFVSGHDSATGEELWRNYFIPRA-----GEEGDETWGNDYEARWMTGAWGQITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VCPTFLGGRDWPSAALNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DSGI-----YFIPLNNVCYDMMAVDQEFTSMDVYNTSNVTKLPPGKDMIGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -WARDTNYQNMIESIDENGI--------VTVNEDAILKEL--DVEYD--
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Pred. No. 6.5e-20;
5; Mismatches 231;
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Q -> H (IN REF. 2).
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R -> L (IN REF. 1).
TLSADATP -> HLKRRCHT (IN REF. 1 AND
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01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUCOSE DEHYDROGENASE-A [PYRROLOQUINOLINE-QUINONE] PRECURSOR (EC 1.1.99.17) (QUINOPROTEIN GLUCOSE DH) (GDH-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1988
01-NOV-1988
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00363; BACTERIAL_PQQ_1; 1. PROSITE; PS00364; BACTERIAL_PQQ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88289368; PubMed=3399393;
Cleton-Jansen A.-M., Goosen N., Odle G., van de Putte P.;
"Nucleotide sequence of the gene coding for quinoprotein glucose
dehydrogenase from Acinetobacter calcoaceticus.";
Nucleic Acids Res. 16:6228-6228(1988).
                                                                                                                                                                                                                                                                                                                                                            CHAIN
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  166
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MISCELLANEOUS: ACINETOBACTER CALCOACETICUS CONTAINS TWO
PQQ DEPENDENT ENZYMES WITH GDH ACTIVITY. GDH-A PREFERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: PQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MONOMER.
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  RGQGEDMVS---
                                                                                                                                                           PAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQITTENVGQLQLVWARGMQPGK 79
                                                                                                                                 PETAQAVPGVAE----SDWPAYGRTQAGVRYSPLKQINDQNVKDLKVAWT--LRTGD
                         HLTCRGVMYYDANNTTEFATSLQSKKSSSTQCPRKVFVPVNDGRLVAVNADTGKACTDFG
                                                                              LKTDNDSGETTNQVTPIKIGNNMFICTAHQQLIAIDPATGKEKW---RFDPKLKTDKSFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S00943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation - burdean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                          169;
                                                                                                                                                                                                                                                                                                                                                                                                                         PF01011; Bacterial_PQQ; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X07235; CAA30222.1;
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                                                                                                                                                                                                      Similarity
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59
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 --NSSGPIVANGVIVAGS-TCQYS--
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POTENTIAL.
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BASE (POTENTIAL.
                                                                                                                                                                                                    Score 390; DB 1;
Pred. No. 9.8e-20;
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                                                                                                                                                                                                                                                                                                                                         [PYRROLOQUINOLINE-QUINONE].
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                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                  Periplasmic;
                                                   -VYFVSWDNHLVALDTATGOVTFDVD
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                                                                                                                                                                                                                 Length 801;
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-PFGCFVSGHDSATG
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P27175;
01-AUG-1992 (Rel. 23, C
01-AUG-1992 (Rel. 23, L
15-DEC-1998 (Rel. 37, L
GLUCOSE DEHYDROGENASE [
                                                                                                                                                                                                                                                                                                                                                                                                                         GLUOX
                                                                                            Submitted (FEB-1992) to -i- CATALYTIC ACTIVITY:
                                                                                                                                                           Cleton-Jansen A.-M., Dekker S., van de Putte P., Goosen "A single amino acid substitution changes the substrate of quinoprotein glucose debydrogenase in Gluconobacter o Mol. Gen. Genet. 229:206-212(1991).
                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=92017653; PubMed=1833618;
                                                                                                                                                                                                                                                                                                Gluconobacter oxydans
                                                                                                                        Goosen
                                                                                                                                                                                                                                                         NCBI_TaxID=442;
                                                                                                                                                                                                                                                                       Gluconobacter
                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                   REVISION TO
                                                                                                                                                                                                                                                                                                                             (E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             796
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                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                              CATALYTIC ACTIVITY:
+ REDUCED ACCEPTOR.
COFACTOR: PQQ.
                         SUBCELLULAR LOCATION: OUTSIDE OF MISCELLANEOUS: THE P1 FORM CAN OX. P2 FORM CAN ALSO OXIDIZE MALTOSE.
  SIMILARITY:
                HERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLP--AGGQATPMTYEINGKQYVVIMAGGHGSFG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTRLATVASGQA--ISYEVDGMQYVAI-AGGGVSYGSGLNSALAGERVDSTAIGNAVYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALP 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKRIGTIRDSLPNLFQLPAVKIGVPGLGGSISTAGNVMFVGATQDNYLRAFNVTNGKKLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNGQVNLQEFMPYAYPGGYNPTSPGIVTGSTVVIAGSVTDNYSNKEPSG-VIRGYDVNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTEQGVQPMYGVPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AILKELDVEYDVCPTFLGGRDWPSAALNPDS-----GIYFI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKTQPFSDLNLAPQDKLTDKDMWGATMLDQLMCRVSFKRLNYDGIYTPPSENGTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AETGEF --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LADIKNKAGQTVPAIYVLTKTGNAFVLDRR--NGQPIVPVTEKPVPQTVKRGPQTKGEFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTNVDVQPSTEMEGLQSINP--NAATGERRVLTGVP----CKTG--TMWQFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASETQRGTPGGTLYG-----TNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLLW--VFDTGAADPNAMPGEGTTFVHNS-----PNAWAPLAYDAKLDIV-YVPTGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EELWRNYFIPRAGE----
                                                                                                                                   213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLNNVCYDMMAVDQEFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                · - - - - - - - LWA - - - - - - - RDTNYQNMI ESIDENG I VTVNED
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
  BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DIWGGDRTELKERYANSMLAINASTGKLVWNFQTTHHDLWDMDVPSQPS
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                                                                                                                                                                                                                                                                                                                                                      . 23, Created)
. 23, Last sequ
. 37, Last anno
                                                                                                                                                                                                                                                                                                                                                      Last sequence up
                                                                                                                                                                                                                                                                                                                                        [PYRROLOQUINOLINE-QUINONE] PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO
                                                                                          the EMBL/GenBank/DDBJ
D-GLUCOSE + ACCEPTOR =
                                      OUTSIDE OF THE PERIPLASMIC MEMBR FORM CAN OXIDIZE ONLY D-GLUCOSE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGDETWGNDYEARWMTGAWGQITYDPVTNLVHYGSTAVGP
                                                                                                                                                                                                                                                                                 alpha subdivision; Acetobacteraceae;
THE
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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 BACTERIAL
                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                           808
                          THE SEQUENCE OF
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 PQQ DEHYDROGENASE FAMILY
                                                                                                                                                                         Gluconobacter oxydans.
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                                                                                          databases.
= D-GLUCONO-1,5-LACTONE
                                                                                                                                                                                     Goosen N.;
ostrate specificity
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                                                     MEMBRANE
                            P1 FORM
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                            NMOHS
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SO PITT

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S17716; QPKEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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LWPEENAKGTGGETGLQHNYGIPYAVNLHPFLDPVLLPFGIKMPCRTPPWGYVAGIDLKT
                                                                                                                                                                                                                   LWARDT -----
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                                                                                       LRYEGPFTPPSLKGSLIFPGDLGMFEWGGLAVDPQRQVAFANPISLPFVSQLVPRGPGNP
                                                                                                                                                                         VPAPETPVPQGAAPGDHTSPTQPMSQ---LTLRPKNPLNDSDIWGGTIFDQMFCSIYFHT
                                                                                                                                                                                                                                                                                                    DQECTFEMMVTNVDVQPSTEMEGLQSINPNAATGERRVLTGVPCKTGTMWQFDAETG-EF
                                                                                                                                                                                                                                                                                                                                              LVYIPMGV-----GTPDQWGGDRTKDSERFAPGIVALNADTGKLAWFYQTVHHDLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYDPKLQINPGFQHLTCRGVSFHETPANAMDSDGNPAPTDCAKDSILPVN-DGRLVEVDA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHRRQL---PNIATLN----SFGE-PTRGMALYGT-----NVYFVSWDNHLVALDT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNVSNLKVAWHIHTKDMMNSNDPGEQTNEATPIEFNNTLYMCSLHQKLFAVDGATGNVKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVLALFASLFTDPHDISGELPTQIANASPADPDNVPASEWHAYGRTQAGDRWSPLNQINA 187
                                                                                                                                                                                                                                                              DMELPSQPSLVDVTQKDGTLVPAIYA----
                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ATQAFDVYTGKRVWVFDASNPDPNQLPDESHPVFHPNSPNSWIVS----SYDANLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGCFVSGHDSATGEELW----RNYFIPRAGEEGDETWGNDYEARWMTGAWGQITYDPVTN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X62710; CAA44594.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                        -EFTSMDVYNTSNVTKLPPGKDMI-----
                                                                                                                                 ----VCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQ-----
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87567
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21.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
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H -> N (IN P2 FORM).
; 0F4160DA78652445 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 340; DB 1;
Pred. No. 3.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLUCOSE DEHYDROGENASE [PYRROLOQUINOLINE: QUINONE].
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                                                                                                                                                                                                                                                                -----PTKTGDIFVLDRRTGKEI 513
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                                          -GRIDAIDIST 472
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Oxidoreductase;
TRANSMEM 14
TRANSMEM 41
                                                                                                                                                                                                                                                                                                                                                                                         Elsemore D.A., Ornston L.N.;

"Unusual ancestry of dehydratases associated with quinate catabolism in Acinetobacter calcoaceticus.";

J. Bacteriol. 177:5971-5978 (1995).

-I- FUNCTION: CAN ACT EITHER ON QUINATE OR ON SHIKIMATE.

-I- CATALYTIC ACTIVITY: QUINATE + PYRROLOQUINOLINE-QUINONE = 5-
DEHYDROQUINATE + REDUCED PYRROLOQUINOLINE-QUINONE.

-I- CATALYTIC ACTIVITY: SHIKIMATE + PYRROLOQUINOLINE-QUINONE.

-I- CATALYTIC ACTIVITY: SHIKIMATE + PYRROLOQUINOLINE-QUINONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            039086;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
00INATE/SHIKIMATE DEHYDROGENASE [PYRROLOQUINOLINE-QUINONE]
PROSITE; PS00363; BACTERIAL_PQQ_1; FALSE_
PROSITE; PS00364; BACTERIAL_PQQ_2; FALSE_
Oxidoreductase; PQQ; Quinate metabolism;
TRANSMEM 14 34 POTENTIAL.
TRANSMEM 41 61 POTENTIAL.
                                                                                                EMBL; L05770; AAC37161.1; -
                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                               use
                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96011389; PubMed=7592351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BD143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-20 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrogenase."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BD143
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Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acinetobacter calcoaceticus
                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The pca-pob supraoperonic cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elsemore D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95095936; PubMed=8002591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   798 DIIAYALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 176:7659-7666(1994).
                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              PATHWAY: QUINIC ACID CATABOLIC PATHWAY; FIRST STEP. THIS PATHWAY ALLOWS GROWTH OF BACTERIA WITH QUINATE BY ITS CONVERSION TO PROTOCATECHUATE AND SUBSEQUENT METABOLISM BY THE BETA-KETOADIPATE
                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: PQQ
                                                                                                                                                                                                                                                                                  INDUCTION: BY
                                                                                                                                                                                                                                                                                                                  PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTTGKVLWQDRLPAGAQATPITYAINGKQYI-----VTYAGGHNSF-----PTRMGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKVVWQHRNGTLRDSMYGSSLPIPLPPIKIGVPSLGGPLSTAGNLGFLTASMDYYIRAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVYVFALP 578
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                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                  PF01011; Bacterial_PQQ;
                                                                                                                                          non-profit institutions as long as its content is in no regulars a license agreement.
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Best Local
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                                                                                      Q9XD78:
Q1-QCT-2000 (Rel. 40, Created)
01-QCT-2000 (Rel. 40, Last sequence update)
01-QCT-2000 (Rel. 40, Last annotation update)
PROBABLE QUINATE DEHYDROGENASE [PYRROLOQUINOLINE-QUINONE]
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SEQUENCE
                            Xanthomonas campestris (pv. juglandis).
Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                    QUIA_XANCJ
 NCBI_TaxID=44291
               Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                    428
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                                                                                                                                                                                                                                                                                                       705 TIQDTGPMGIKMGLKAPIGMPTIGGPMATQGGLVFFAATQDYYLRAFNSSNGKELWKARL
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                                                                                                                                                                                                                                                                                                                                                                                                                             GLYTAPGTDVSLSFPGSLGGMNWGSIAFDPTHRYMFVNDMRLGLWIQLIKQTPEDIKIQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVDGRLIAVNADTGARCKDFGVNGTVNLHEGLGENTKAPRFEVTSAPTIAGTTIVVGSRI 365
                                                                                                                                                                                                                                                                                                                                                                  NGGEKVNTGMGAVPMKGTPYKVNKNRFMSALGIPCQKPPFGTMTAIDMKTRQVAWQVPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------WARDTNYQNMIESIDENGIVTVNE------DAILKELD---VEYD 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECTFEMMVTNVDVQPSTEMEGLQSINPNAATGERRVLTGVPCKTGTMWQFDAETGEFL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVTNLVH --YGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADNVAADMPGGVIRAYDVITGKLRWA--FDPRNPDPNYVLKPGEIYKRSSTNSWAAMSYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTSLLWASAGALALLAA-PAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQITT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----FDLPMQPS-----LVDFPMKDGTTKPAVVIGT--KSGQFYVLDRVTGKPLTK 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AEVNSTADAWERCRGVAYFDSTQPLVQPTLAGATPVAALAANTECPRRVYTN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENVGQLQLVW-----ARGMQPG-KVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VCPTFLGGRDWPSAALNPDSGIYF----
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110 P
147 P
88196 MW;
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Pred. No. 2.2e-14;
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71F67CEBEA62BFCB CRC64;
                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                  PVLSTGGGVLFNGGTDRYFRALSQETGETLWQTRL
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                            Xanthomonas group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A gene involved in quinate metabolism is specific to one E group of Xanthomonas campestris.";
J. Appl. Microbiol. 87:649-658(1999).
-!- CATALYTIC ACTIVITY: QUINATE + PYRROLOQUINOLINE-QUINONE DEHYDROQUINATE + REDUCED PYRROLOQUINOLINE-QUINONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; PQQ; Quinate metabolism; TRANSEM 22 42 POTENTIAL. TRANSMEM 48 68 POTENTIAL. TRANSMEM 77 94 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00363; BACTERIAL_PQQ_1; FALSE_NEG PROSITE; PS00364; BACTERIAL_PQQ_2; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: PQQ (BY SIMILARITY).

-!- PATHWAY: QUINIC ACID CATABOLIC PATHWAY; FIRST STEP. THIS PATHWAY
-INTERPRETARY AND SUBSEQUENT METABOLISM BY THE BETA-KETOADIPATE
PROTOCATECHUATE AND SUBSEQUENT METABOLISM BY THE BETA-KETOADIPATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
STRAIN=C5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20063481; PubMed=10594704;
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   484
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IGTKAGQIYVLDRATGKPLTEVREVPVKGSDIAHEQYAPTQPLSVGMPQIGTKHLTESDM
                                   VPCKTGTMWQFDAETGEFLW-ARDT-----NY---QNMIESIDENGIVTVNEDAI
                                                                                                                                                                                                                                                                                                                                                                                          LIWEHRRQLPNIATLNSFGEPTRGMALY-----
                                                                      DATTGAEKWYYQTVHNDLWD-
                                                                                                       RPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSINPNAATGERRVLTG
                                                                                                                                                                                                                TRADDNVQTDMPGGVVRG-----SMWSP--VRSAGLDP----GNPHDRQAPAAGSSYV 390
                                                                                                                                                                                                                                               T-----CQYSPFGCFVSGHDSATGEELWRNYFIPRAGEEGDETWGNDYE------A
                                                                                                                                                                                                                                                                                 {\tt FINTIDGRLIAVDADTGAFCQGFGSNGQVDLKAGLGAAPDPFYQLTSPPLVAGTTVVGGR}
                                                                                                                                                                                                                                                                                                                      YFVSWDNHLVALDTAT-----
                                                                                                                                                                                                                                                                                                                                                       QLW--RRE---INATSSVWQRCRGLGYFDADAALPAPSVANPSPIAAVTVAQGANCRRRL
                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt NRSN-GRPAAGSPGPTTPGEIANSDGNGAEDQLTPLQVGEKVFLCTPHNNLIALDASTGK}
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTENVGQLQLVWARGMQPGKV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASAGALALLA--APAFAQVTPVTDE----LLANPPAG---EWISYGQNQENYRHSPLTQI 59
                                                                                                                                            RSTPNVWAPMSYDAAMNTVF----
                                                                                                                                                                           RWMTGAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATVLALAVVAGIGGMFVPHPPVAGNAGPGMTAVPPGSVQQNWSAYGNTDGGSRFAALDQI 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              790 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Yu P.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%;
22.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 276;
Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                    -GQVTFDVDRGQGED-MVSNSSGPIVANGVIVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B75F29B52A49FE6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                  FDLPMQPSL-----
                                                                                                                                          -LPLGGPSTDLYGAERTALDHRYGASVLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QVTPLIHDGVMYLANPGDVIQAIDAKTGD 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 236;
                                                                    IDFPNQDGSHTPAVV
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망	Qy	Дb	Qy	Дb	Qy	Db	Qy	Db	Qy
773	557	720	500	663	459	604	425	544	392
773QSPDRGDYVIAYSLP 787	557 ALAGERVDSTAIGNAVYVFALP 578	720 AGTQDYYLRAFDSATGKELMKGRLFVGSQGGPITYVSHKTGKQYVVISAGGAR 772	500 GGT-DRYFRALSQETGETLWOTRLATVASGQAISYEVDGWQYVAIAGGGVSYGSGLNS 556	663YGTLSAIDLKTRSIAWQVPVGTVQDTGPFGIKMHLPIPIGMPTLGGTLSTQGGLVFI 719	ERAAANYSPV	604 MRLGLWVQMIPADTRKAEAAGGGEAVNTGMGAVPLKGTPYAVNKNRFLSALGIPCQAPP- 662	425PDLNNPCYDMMAVDQEFTSMDVYNTSNVTKLPPG 458	544 WGATAMDQMLCRIAFKQMRYEGLYTAPGTDVSLSFPGSLGGMNWGGLSTDPVHDVVFAND 603	392 LKELDVEYDVC

Search completed: August 8, 2001, 19:44:11 Job time: 183 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
   SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fund::*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe!1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_unclass:
13: sp_vertebr:
14: sp_virus:**
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3089
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Gapop 10.0 , Gapext 0.5
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sp_plant:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
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sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
,	616	19.9	869	Ν	Q9КН03	Q9kh03 alcaligenes
2	583	18.9	708	Ν	Q46444	Q46444 comamonas t
w	561	18.2	742	N	Q53362	Q53362 acetobacter
4	560	18.1	601	N	Q9EYW8	Q9eyw8 rhizobium m
5 1	549.5	17.8	695	N	Q9F9U2	Q9f9u2 pseudomonas
0	537.5	17.4	601	N	P71509	P71509 methylobact
7	479.5	15.5	633	ν	024759	024759 hyphomicrob
8	473	15.3	599	N	Q9L935	Q91935 methylovoru
9	439.5	14.2	573	Ν	Q59540	Q59540 methylophil
10	365.5	11.8	790	Ν	Q9X2S5	Q9x2s5 pantoea cit
11	327	10.6	803	2	Q91115	
12	324.5	10.5	786	N	P95466	P95466 pantoea cit
13	281.5	9.1	644	N	Q52551	Q52551 pseudomonas
14	276.5	9.0	639	N	P77931	P77931 pseudomonas
15	218	7.1	470	2	030326	030326 acetobacter
16	208.5	6.7	182	2	032699	032699 hyphomicrob
17	203.5	6.6	179	Ŋ	032697	032697 hyphomicrob
18	200.5	6.5	180	N	032700	O32700 hyphomicrob
19	200.5	6.5	180	ν	032696	032696 hyphomicrob

	44 1																									
67.5	167.5	67.5	68.5	68.5	169	69.5	72.5	74.5	81.5	82.5	.83.5	185	85.5	85.5	86.5	86.5	90.5	91.5	91.5	93.5	95.5	96.5	97.5	99.5	00.5	
5.4	.4	5.4	G	5	5	ഗ	o	.6	.9	.9	.9	.0	.0	.0	.0	.0	.2	. 2	.2	w	ω	. 4	. 4	.51	·.	
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xyiella las	ac	unidentifie	environment	unidentifie	thiobacillu	uncultured	uncultured	hyphomicrob	uncultured	hyphomicrob	hyphomicrob	methylosinu	hyphomicrob	hyphomicrob	hyphomicrob	methylosinu	hyphomicrob	hyphomicrob	hyphomicrob	hyphomicrob	hyphomicrob	nyphomicrob	hyphomicrob	hyphomicrob	hyphomicrob	

ALIGNMENTS

da g	OV.	Db	Qy	Db	Qy			SQ	DR	DR	DR	DR	DR C	Z 7	R R	RP	RN.	2 8	18	SO	J [DI	DI AC	ID	20	R
8 -	<	σ	×	σ	Υ.	Best	Que								•										KHO	RESULT
134	v 124 LNSFGEPTRGMALYGTNVYFVSWDNHLVALDTATGQVTFDVDRGQGEDMVSNSSGP	74	y 66 QLQLWARGMQPGK-VQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLP-NIAT 123	14 AAASVALPAPMAFGANAAARVDGAAIRANEAGTPNWPSYGLDYAETRESKLEQVNAGNVR	10	Best Local Similarity 30.3%; Pred. No. 2.8e-35; Matches 186; Conservative 93; Mismatches 247;	Query Match 19.9%; Score 616	SEQUENCE 698 AA; 75471 MW;	PROSITE;		InterPro;			Submitted (JUN-2000		SEQUENCE FROM N.A.		RAISTONIA.			TERAHYDROFURFURYL ALCOHOL D	01-OCT-2000 (TrEMBLrel. 15,	01-OCT-2000 (TrEMBLrel. 15, Created)	Q9KH03 PRELIMINARY; PRT;		SULT 1
: :: : : ATGKKVWEQDTIVDRSKSYTITGAP 190	ATGQVTFDVDRGQGEDMVSNSSGP 179	WSVVHAIDARTGKRLWTYDPQVPRDQAY 133	GDVIQAIDAKTGDLIWEHRRQLP-NIAT 123	TPNWPSYGLDYAETRESKLEQVNAGNVR 73	EWISYGQNQENYRHSPLTQITTENVG 65	. 2.8e-35; tches 247; Indels 88; Gaps	6; DB 2; Length 698;	9C87F180DB1D2FB2 CRC64;	NN_1.				,	ank/DDBJ databases.	rufa-DH.":				ision; Raistonia group;		EHYDROGENASE.	Last sequence update)		698 AA.		

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ACCOMPANDA 
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Biochem.
                                               Groen B.W., van Kleef M.A., Duine J.A., "Quinohaemoprotein alcohol dehydrogenase
                                                                                                                                                                                Purification, characterization, and reconstitution with pyrroloquinoline quinone analogues."; Eur. J. Biochem. 230:899-905(1996).
                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 15667;
MEDLINE=95324580; PubMed=7601151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of the gene encoding quinohaemoprotein ethanol dehydrogenase of Comamonas testosteroni.";
Eur. J. Biochem. 235:690-698(1996).
                            testosteroni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 15667;
MEDLINE-96184549; PubMed-8654419;
Stoorvogel J., Kraayveld D.E., van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comamonas testosteroni (Pseudomonas testosteroni).
Bacteria; Proteobacteria; beta subdivision; Comamo
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
QUINOHAEMOPROTEIN ETHANOL DEHYDROGENASE TYPE I PRECURSOR
                                                                                                       CHARACTERIZATION.
MEDLINE=86242113; PubMed=3521592;
                                                                                                                                                                                                                                      Duine J.A.;
"Quinohaemoprotein ethanol dehydrogenase from Comamonas to
                                                                                                                                                                                                                                                                                                                                De Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Vries S., Duine J.A.;
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                                                                                                                                                                                                                                                                                                                             G.A.H., Geerlof
  ۲.
234:611-615(1986).
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                                                                                                                                                                                                                                                                                                                       Α.,
                                                                                                                                                                                                                                                                                                                       Stoorvogel J., Jongejan J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sluis C.A.,
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PROSITE; PS00364; BACTERIAL_PQQ_2; 1.
Signal; PQQ; Heme; Calcium; Oxidoreductase;
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-!- SIMILARITY: TO ALCOHOL DEHYDROGENASE (ACCEPTOR) PROTEINS EMBL; X81880; CAA57464.1; -.
HSSP; P38539; 4AAH.
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Pfam; PF01011; Bacterial_PQQ; 6.
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InterPro; IPR002372; -.
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COFACTOR: PQQ, HEME, AND CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION:
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FQGTADGRLVAYHAATGEKLWEAPTGTGVVAAPSTYMVDGRQYVSVAVGWGGVYG---
                                                  FNGGTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAIA-GGGVSYGSGLNS
                                                                                                          GKPQSGTGWNTAKFFNAEPPKSKPFGRLLAWDPVAQKAAWSVEHVSPWNGGTLTTAGNVV
                                                                                                                                                                                                                                                                    EDAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQ-EFT----
                                                                                                                                                                                                                                                                                                                                                                               QSINPNAATGERRYLTGYPCKTGTMWQFDAETGEFLWARDTNYQNMIESIDENG-IVTVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDRGQGEDMVSNSSGPIVANGVIVAGST-CQYSPFGCFVSGHDSATGEELWRNYFIP---
                                                                                                                                                                                                               -- AAARDGSKPQDAVPGPYGAHNWHPMSFNPQTGLVYLPAQNVPVNLMDDKKWEFNQAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                    RSPKGGDNLYLASIVALDPDTGKYKWHYQETPGDNWDYTSTQPMILADIKI------
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6.1e-33;
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Best Local
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Pfam; PF01011; BacterIal_PQQ; 6.
PROSITE; PS00363; BACTERIAL_PQQ_1; 1.
PROSITE; PS00364; BACTERIAL_PQQ_2; 1.
SEQUENCE 742 AA; 81680 MW; 031C4E9B6B13EC98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takemura H., Kondo K., Horinouchi S., Beppu T.;
"Induction by ethanol of alcohol dehydrogenase activity in
pasteurianus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-CCT-2000 (TIEMBLIEL. 15, Last annotation update)
DEHYDROGENASE SUBUNIT OF ALCOHOL DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q53362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q53362; Q44159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 175:6857-68
EMBL; D13893; BAA40252.1;
HSSP; P38539; 4AAH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AGALALLAAPAFAQVTPVTDELL--ANPPAGEWISYGQNQENYRHSPLTQITTENVGQLQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
               VDQEFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSVERAAANYSPVLSTGGGV
                                               GLYTLTGKFWYGIPGPLGAHNFMGMAYSPKTHLVYLPAHQIPFGYKNQVGGFKPHPDAWN 471
                                                                               AILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCY-----
                                                                                                                                                                              GIGSNLFLGSIVALKPETGEYVWHFQATPMDQWDYTSVQQIMTLDMPV------
                                                                                                                                                                                                                                          YKTWGP--KGAWVRQGGGGTVWDSLVYDPVSDLIY---LAVG----NGSPWNYKYRSE
                                                                                                                                                                                                                                                                       -ETWGNDYEARWMT----GAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLY---
                                                                                                                                                                                                                                                                                                         VAKGLVLIGN--GGSEFGARGFVSAFDAETGKLKWRFYTVPNNKNEPDHAVADNVLMSKA
                                                                                                                                                                                                                                                                                                                                         VANGVIVAGSTCQYSPFGC--FVSGHDSATGEELWRNYFIPRAGEEGD------
                                                                                                                                                                                                                                                                                                                                                                         CDTVNRGAGYWNGKVFWGTFDGRLVAADAKTGKKVWEVNTIPADASLGKQRSYTVDGAVR 202
                                                                                                                                                                                                                                                                                                                                                                                                        FGEPTRGMALYGTNVYFVSWDNHLVALDTATGQVTFDV-----DRGQGEDMVSNSSGPI- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                        LAWYYTLDTNRGQEATPLVVDGIMYATTNWSKMEALDAATGKLLWQYDPKVPGNIADKGC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVWARGMQPGKVQ-VTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLP-NIATLNS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt AAALPYAAVPARADGQGNTGEAIIHADDHPENWLSYGRTYSEQRYSPLDQINRSNVGDLK}
                                                                                                                                            NPNAATGE-RRVLTGVPCKTGTMWQFDAETGEFLWARDTNYQNMIESIDE-NGIVTVNED 389
                                                                                                                                                                                                              --GTN---
                                                                                                               ----NGEMRHVIWHAP-KNGFFYVLDAKTGEFLAGKNYVYQNWANGLDPLTGRPIYNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175:6857-6866(1993).
                                                                                                                                                                                                          TRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSI 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.2%;
28.5%;
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<del>-</del> ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 561; DB 2; Pred. No. 2.4e-31;
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RESULT
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Best Local :
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"Regulation of Cl assimilation in Sinorhizobium meliloti.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF309488; AAG31643.1;
SEQUENCE 601 AA; 65686 MW; 09F743726B2E2A83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9EYW8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MXAF'.
Rhizobium meliloti (Sinorhizobium meliloti).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RM1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 LALLAAPAFAQVTPVTDEL--LANPPAGEWISYGQNQENYRHSPLTQITTENVGQLQLVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFQGLANGEFHAYDATNGSDLYKFDAQSGIIASPMTYSVNGKQYVAVEVGWGGIYPISMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVGRTSG
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                                                                                                                                                                                                                                 VRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSINPNAATGERRVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ARGMQPGKVQVTPLIHDGVMYLANP-GDVIQAID-AKTGDLIWEHR-RQLPNIATLNS 126
GQPYVGATLSMYPP-KDSHGGMGNFIACDNKEGKIKWSLPEPFSVWSGALATAGDVVFYG
                                                                                                                                                                 GVPCKTGTMWQFDAETGEFL------WARDTNYQNMIE------SIDENGI
                                                                                                                                                                                                                                                                     TWEGD---QWKIGGGTTWGWYSYDPEENLYYYGTGNPSTWNPTQR--PGDNRW-SMTIFA
                                                                                                                                                                                                                                                                                                     TWGNDYEARWMTG----AWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFA
                                                                                                                                                                                                                                                                                                                                         LVGISGGEFGVRG-HVTAYSMADGKVLWRGYSMGPDSDTLIDPEKTTHLGKPVGKDSGLT
                                                                                                                                                                                                                                                                                                                                                                         IVAGSTCQYSPFGCFVSGHDSATGEELWRNYFI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FGEPTRGMALYGTNVYFVSWDNHLVALDTATGQVTFDVDRGQGEDMVSNSSGPI-VANGV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFSTGVLRGH-EGSPLVIGDLMYVHTPFPNTVYALDLSKDGQIVWKYEPKQDPNVIPVMC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAIMSIGGGAQVAFANDELQKLIDDP-NQWAIQTGDYANLRYSKLDQINKDNVGKLQVAW
                                MDVYNTSNVTKLPPGKDM----IGRIDAIDISTGRTLWSVERAAANYSPVLSTGGGVLFNG 500
                                                                                                 VTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQEFTS
                                                                                                                                   HFD-RNGFGYTMDRVTGELLVAEKYDPTVNWATEVVMDPKSDKYGRPQVVAQYSTEQNG-
                                                                                                                                                                                                   RDVDTGMAKWLYQMTPHDEWDYDGVNEMILTGQHIDGK------
                                                                 EDTNTT-----GVCPAALGTKDQQPAAYSPKTELFYVPTNHVCMDYEPFRVSYTA
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27.1%; Pred. No. 2e-31;
tive 109; Mismatches 2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and characterization of genes chloroethanol in Pseudomonas stutzeri BC-2."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ EMBL; AF176640; AAG09249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang C.-H., Herrick J.B., Okinaka R.T., Terwilliger T.C.;
                  467
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            AIDISTGRTLWSVERAAANYSPVLSTGGGVLFNGGTDRYFRALSQETGETLWQTRLATVA
                                                                                                                                                                                                    KLGGGGTVWDSMAYDPELDLLYIGTGNGSPWNREIRSPGGGDNLYLSSILALRPDSGKLL
                                                                                                                 WQFDAETGEFLWARDTNYQNMIESID--ENGIVTVNEDAILKELDVEYDVCPTFLGGRDW
                                          HSMSFNPQTGLMYIPYQEIPGVYRNEGATFKKIDGLNTGTGFSDTHEIP--RDAVSGALL
                                                                 PSAALNPDSGIYFIPLNNVCYDMMAVDQEFTSMDVYNT----SNVTKLPPGKDMI-GRID
                                                                                             YVLDRATGELLSAEKFGKVTWAEKVDLATGRPVEVPGSRYEKEQVVMW----PSSFGAHNW
                                                                                                                                                 WHYQTTPGETWDFTATQQITLATL-----ELDG-----KPRKVLMQAP-KNGFF
                                                                                                                                                                          WRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSINPNAATGERRVLTGVPCKTGTM
                                                                                                                                                                                                                              MTG----AWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIV
                                                                                                                                                                                                                                                         GGAEYGVRG-FFSAYDAETGKMAWRFYTVP--GDPAQPYEHPELAEAAKTWKGDQY---W
                                                                                                                                                                                                                                                                                  STCQYSPFGCFVSGHDSATGEELWRNYFIPRAGE------EGDETW-GNDYEARW
                                                                                                                                                                                                                                                                                                                                      TRGMALYGTNVYFVSWDNHLVALDTATGQVTFDVDRGQGEDMVSNSSGPIVANG-VIVAG
                                                                                                                                                                                                                                                                                                                                                                 LDLENNRGLEATPLVSDGVLYASLSWSRVMAVDLRSGKRLWQFDPQVDRGHSRYTCCDAV
                                                                                                                                                                                                                                                                                                                                                                                                                      ALLVA-AGAQAAKVDEAAIRASEQDGSEWLSHGRTYAEQRFSPLKQIDAGNVGKLGLAWY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                              ALLAAPAFAQVTPVTDELL--ANPPAGEWISYGQNQENYRHSPLTQITTENVGQLQLVWA 72
                                                                                                                                                                                                                                                                                                              NRGVALWNGKVYVGALDGRLIALDAKTGRELWSEQTTDPAKPYSITGAPRVVKGKVIIGN
                                                                                                                                                                                                                                                                                                                                                                                          RGMQPGK-VQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLP-NIATLNSFGEP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLEGYLKAVDAATGKELYRFKTPSGVIGNVMTYAREGKQYVAVLSGVGGWAGIGLAAGLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168;
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roteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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(TrembLrel. 16, Last seq
(TrembLrel. 16, Last ann
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75842 MW; D29A698A642E1A83 CRC64;
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29.2%;
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Last annotation updat
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9; Mismatches
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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PROSITE; PS00364; BACTERIAL_PQQ_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P38539; 4AAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 558 LAG-----ERVDSTAIGNAVYVFALP 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         503
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                                                                                                                                                                                                                               190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGFLKAVDSKTGKELYKFKTPSGIIGNVMTYEHKGKQHVAVLSGVGGWAGIGLAAGLTDP 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQLKHAWS--FSTGELHGHEGAPLVIGDMMYVHSSFPNKTFALNLNDPGHILWQHSPKQD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMSASCMAIAVALQVGVASSAYANDKLIELSKSNENWVMPGKNYDSNNYSESTQVNAENV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLWASAGALALLAAPAFAQVTPVTDELLANPPAGE-WISYGQNQENYRHSPLTQITTENV 64
                                                                                                                                                                        --PRAGEE--GDETWGNDYEARWMTGA---WGQITYDPVTNLVHYGSTAVGPASETQRGT
                                                                                                                                                                                                                                                                                         VSNSSGPIVANGVIVAGSTCQYSPFGCFVSGHDSATGEELWRNYFI------
                                                                                                                                                                                                                                                                                                                                                   PAARSVACCDLVNRGLAYWPGDDKTPALVIKTQLDGHLVALNAKTGEEFWKVENGDIKVG 189
                                                                                                                                                                                                                                                                                                                                                                                                    PNIATLNSFGEPTRGMALYGTN------VYFVSWDNHLVALDTATGQVTFDVDRGQGEDM 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQLQLVWARGMQPGKV---QVTPLIHDGVMYLAN--PGDVIQAIDAKTGDLIWEHR-RQL 118
                                                                                                                 ANPHYGQKGLGTATWEGD---AWKIGGGTNWGWYAYDPQANLIYYGSGNPAPWNETMR--
                                                                                                                                                                                                                                  QTLTQAPYVVHDLAIVGSSGAELGVRGHVTAYNVKTGEQAWRYYATGPDEEIGLADDFNS
PGDNKW-TMTITARDADTGKMKFGYQKTPHDEWDFAGVNVIMLSE-----QTDKE----
                                                       PGGTLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSI\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633 AA; 69852 MW;
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25.0%;
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xidation genes in the methylotroph
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RESULT
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Q9L935;
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TIEMBLIEL. 15, Created)
01-OCT-2000 (TIEMBLIEL. 15, Last sequence update)
01-MAR-2001 (TIEMBLIEL. 16, Last annotation updat
METHANOL DEHYDROGENASE LARGE SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01011; Bacterial_PQQ; 7.
PROSITE; PS00364; BACTERIAL_PQQ_2;
SEQUENCE 599 AA; 65133 MW; DBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1999) to the EMBL/GenBank/DDBJ EMBL; AF184915; AAD56237.2; -. InterPro; IPR001479; -. InterPro; IPR002372; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and nucleotide sequence of mxaF gene of Methylovorus strain SSI DSM11726.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methylovorus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methylovorus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=81683;
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                                                                183
                                                                                                                              123
                                                                                                                                                             118
 241 HYGQMGLGTKTWEGE---GWKIGGGTNWGWYAYDPKLNLFYYGSGNPAPWNETMR--PGD
                                                                                                                                                                                           64
                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                     4 TSLLWASAGALALLAAPAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQITTEN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQYVAIAGG-----GVSYGSGLNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPNAATGERRVLTGVPCKTGTMWQFDAETGEFLWA----RDTNYQNMIESIDENGIVTVNE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTAGLGAVGAFKNLQRY--TQMGGSLEVFSL 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDGFLKARNSDTGELLWKHKLPSGVIGYPMTYEHKGVQYIAVMSGVGGWPGVGLVFDLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt PEFGTRMDHKGTEICPSAMGYHNQGHDSYDPTKQLFFMGINHICMDWEPFMLPYRAGQFF}
                                                                                                                                                           LPNIATLNSFGEPTRGMALYGTNVYFVSWDNHLVALDTATGQVTFDVDRGQGEDMVSNSS 177
                            RAGEE - - GDETWGNDYEARWMTGA - - - WGQITYDPVTNLVHYGSTAVGPASETQRGTPGG
                                                                                            GPIVANGVIVAGSTCQYSPFGC--FVSGHDSATGEELWRNYFI-------
                                                                                                                             DASVKAVACCDIVNRGLAYDDGHIFKTQLDGHLVASDAKTGKELWKMENCDPAVGSTITQ 182
                                                                                                                                                                                           VKNLESGLGHFSTGLLTGH-EGAPLVIGDMMYINTPFPNNTFALNLAEPEKIVWQHKPKQ
                                                                                                                                                                                                                        VGQLQL---VWARGMQPGKVQVTPLIHDGVMYLAN--PGDVIQAIDAKTGDLIWEHR-RQ 117
                                                                                                                                                                                                                                                        TATGFAVAGLALSAMLPSVAAAADSLEALGANP--NNWTMQTGDYTGQHYSRLSQITTGN
                                                                APFAVKGKVLVG--CSGAELGVRGYVTAYDQKTGELVWRSFATGPDNELNLAKDFNKDNP
                                                                                                                                                                                                                                                                                                                        157;
                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                       15.3%;
                                                                                                                                                                                                                                                                                                                          108;
                                                                                                                                                                                                                                                                                                                                         Score 473; DB 2;
pred. No. 2.8e-25;
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                                                                                                                                                                                      Matches 146;
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Best Local
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SEQUENCE 573 AA;
                                                                                                                                                                                                                                                                                     InterPro; IPR001479; -.
InterPro; IPR002372; -.
Pfam; PF01011; Bacterial_PQQ; 7.
PROSITE; PS00304; BACTERIAL_PQQ_2; 1.
                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: PQQ.
EMBL; U41040; AAA83765.1;
HSSP; P38539; 4AAH.
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1995) to the EMBL/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methylophilus methylotrophus (Bacterium W3A1),
Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
Methylophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-MAY-2000 (TREMBLrel. 13, Last annotation update)
METHANOL DEHYDROGENASE HEAVY SUBUNIT (EC 1.1.99.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xia Z.X., Dai W.W., Zhang Y.F., He Y.N., White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q59540
132 LDAKTGKINWEVEVCDPKVGSTLTQAPFVAKDTVLMG--CSGAELGVRGAVNAFDLKTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mathews F.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-W3A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     059540;
                            153 LDTATGQVTFDVDRGQGEDMVSNSSGPIVANGVIVAGSTCQYSPFGC--FVSGHDSATGE
                                                                                     94 ANPGDVIQAIDAKTGDLIWEHR-RQLPNIATLNSFGEPTRGMALYGTNVYFVSWDNHLVA 152
                                                                                                                           13
                                                                                                                                               38 AGEWISYGQNQENYRHSPLTQITTENVGQLQLVW--ARGMQPGKVQVTPLIHDGVMYL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518
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                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 REDUCED ACCEPTOR.
                                                         AFPNNTYALNINDPGKIVWQHKPKQDASTKAVMCCDVVDRGLAYGAGQIVKKQANGHLLA
                                                                                                                      AGAWPIATGGYYSQHNSPLAQINKSNVKNVKAAWSFSTGVLNGH-EGAPLVIGDMMYVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ERVDSTAIGNAVYVFAL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKLP----PGKDMIGRIDAIDISTGRTLWSVERAAANYSPVLSTGGGVLFNGGTDRYFRA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLYGTNTRFAVRPDTGEIVWRHQTLPRDNWDQECTFEMMVTNVDVQPSTEMEGLQSINPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGAFKELQNYTQMGGGVMVFGL 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDKTNGKEIWKFKMPSGAIGAPMSYAYKGKQYIATNYGVGGWPGVGLVFDLTDPSAGLGA 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSQETGETLWQTRLATVASGQAISYEVDGMQYVAI---AGG--GVSYGSGLNSALAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMYPGPNGPTKKEMGQVLAMDGVTGEVKWTKWEKFSVWGGTLATKGGLVFYNTLDGNIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt RMDHKGTNICPSAMGFHNQGLDAYDPDSRTFYFGLNHICMDWEPFMLPYRAGQFFVGATL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELDVE-YDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQEFTSMDVYNTSNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGERRVLTGVPCKTGTMWQFDAETGEFLWARDTN-YQNMIESIDENGIVTVNEDAILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKW-TMTIWARDVDTGAAKWGYQKTPHDEWDFAGVNQMILTDQAVNGKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PLLTHVD-RNGIMYTLNRQTGSIVQAAKVDPAVNVFKKVDLKTGLPVRDPEFST 397
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ACCEPTOR))
                                                                                                                                                                                                                                                           62635 MW; A06C9B3091BB8F0C CRC64;
                                                                                                                                                                                              14.2%;
24.5%;
                                                                                                                                                                                   99;
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                 Score 439.5;
Pred. No. 6e
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               ALCOHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573
                                                                                                                                                                                                6e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        G.D.,
                                                                                                                                                                                 93;
                                                                                                                                                                              Gaps
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Best Local S
                                                                                                                                                                                                                                                                                                                                                Matches
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Q9X2S5;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "gdhB, a gene encoding a second quinoprotein glucose dehydrogenase Pantoea citrea, is required for pink disease of pineapple."; Microbiology 145:1217-1226(1999).
EMBL; AFOS0503; AAD23735.1; -.
InterPro; IPR001479; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002372; -.
Pfam; PF01011; Bacterial_PQ0; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pujol C.J., Kado C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=1056R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=53336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99303331; PubMed=10376838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pantoea citrea
           266
                                                             137
                                                                                                               209 ITNESTPLKVGNLLYTCTAHQILVAIDAATGKEKW----RFDPKIKYDPTFQHMTCRGVSY
                                                                                                                                                                                                                                 152
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HDFNTATDPQSAPVSPAACSRRIYLPVNDGRLIAVDAENGQLCKDFGNNGELDLQHQQPN
                                                             YGTN----
                                                                                                                                                                V--QVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPNIATLNSFGEPT-RGMAL 136
                                                                                                                                                                                                                        PATQPVSAGK----DWTAYGGTQAGDRYSSLSQINESNVKNLQVAWTYQSGDVKRPDDPGE
                                                                                                                                                                                                                                                                            PVTDELLANPPAGEWISYGQNQENYRHSPLTQITTENVGQLQLVWA------RGMQPGK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYVAIAGGGVSYGSG------LNSALAG-----ERVDSTAIGNAVYVFAL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KWEKFAAWGGTLYTKGGLVWYATLDGYLKALDNKDGKELWNFKMPSGGIGSPMTYSFKGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYAGLNHICMDWEPFMLPYRAGQFFVGATLAMYPGPNGPTKKEMGQIRAFDLTTGKAKWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKWRAFATGSDDSVRLAKDFNSANPHYGQFGLGTKTWEGD---AWKIGGGTNWGWYAYDP
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                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00364; BACTERIAL_PQQ_2; 1.
790 AA; 85681 MW; 88BB7625E0A5F089 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                790 AA;
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
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23.9%;
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                                                    -VYFVSWDNHLVALDTATGQVTFDVDRGQGEDM-----
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 365.5;
                                                                                                                                                                                                                                                                                                                                             Mismatches
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Matches 166;
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                                                                                                                                                                                                                                                                                                      MEDLINE-20437337; PubMed=10984043; Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Lagrou M. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel.
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Nature 406:959-964(2000).
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                                                                                                                                                                                                 AE004654; AAG05678.1; -. Pro; IPR002372; -.
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                                           STRAIN-1056R;
                                                                                                              Bacteria; Proteobacteria;
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                            MEDLINE=97133947; PubMed=8979341;
                                                         SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------LPPGKDMIGRIDAIDISTGRTLWSVERAAA-NYSPV-----
                                                                                                                                citrea.
                                                                                                                                                         1997 (TremBLrel. 03, Last sequence update)
2000 (TremBLrel. 14, Last annotation update)
DEHYDROGENASE [PYRROLOQUINOLINE-QUINONE] (E
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                                                                                                                                                                                                     (TrEMBLrel. 03, Created)
                                                                                                                                                                                                                                 PRELIMINARY;
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                                                           AND ACTIVITY
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    Pantoea
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    citrea
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ACT_SITE
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PROSITE; PS00363; BACTERIAL_PQQ_1; 1.
PROSITE; PS00364; BACTERIAL_PQQ_2; 1.
Oxidoreductase; PQQ; Transmembrane; Periplasmic.
495 FVLNRDTGKPVVPAPETPVPQGPAKGDHLSPTQPFSELTFRPKNKLQGRDMWG-ATMFDQ
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-i- MISCELLANEOUS: RESPONSIBLE FOR PINK TO BROWN DISCOLORATIONS OF INFECTED PINEAPPLES UPON HEATING DURING THE CANNING PROCEDURE INFECTED BATCHES HAVE TO BE DISCARDED.
-i- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY X95985; CAA65229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl. Environ. Microbiol -i - CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pineapple.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucose dehydrogenase that is essential for causing pink disease
                            354
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InterPro; IPR002372;
                                                                                                                                                                               194
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                                                                         DNW----DQECTFEMMVTNVDVQPSTEMEGLQSINPNAA-----TGERRVLTGVPCKTGTM
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                           WQFDAETGE-FLWARDT-----
                                                VYWLCMPQLASWHGFTRRYTMQSFWDMD-LPS-QPTLADITDEQGKTVPVVYVPAKTGNI
                                                                                                   PAAYDAQRDIIYLP----
                                                                                                                         QITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDT--GEIVWRHQTLPR
                                                                                                                                                                                                                           DNHLVALDTATGQVTFDVDRGQGEDMVSN-----SSGPIVANG-VIVAGSTCQ 193
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                                                                                                                                                  NLSTREPSG-VIRGEDIDSGKLLW--VFDPGAKDPNAVPADGQTFVANS-----PNSWA
                                                                                                                                                                          ----YSPFGCFVSGHDSATGEELWRNYFIPRAGE-----EGDETWGNDYEARWMTGAWG
                                                                                                                                                                                                  DGRLFAVDALTGQRCSNF-ANNGELNLQHLQPNAYPGGYEPTSPPIITDKVVIIAGSVTD
                                                                                                                                                                                                                                                                          IQAIDAKTGDLIWEHRRQLPNIAT-------LNSFGEPTRGMALYGTNVYFVSW
                                                                                                                                                                                                                                                                                                   EGVRYSPLTQINDKNVQQLQVAWQFHTGDHKTANDPGEITNEVTPLKVGNMLYLCTPHQI
                                                                                                                                                                                                                                                                                                                          ENYRHSPLTQITTENVGQLQLVW-----ARGMQPGKV--QVTPLIHDGVMYLANPGDV
                                                                                                                                                                                                                                                                                                                                                    KPLLAMVIGLGINALLLLGASLHDPQEINGVLNVSDK----PPAESAASAADWPAYGRTQ 170
                                                                                                                                                                                                                                                                                                                                                                             KPTSLLWASAGALALLAAPAFAQ-----VTPVTDELLANPP-----AGEWISYGQNQ
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86038 MW;
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Pred. No. 1.3e<sup>-</sup>
91; Mismatches
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PQQ-BINDING.
BY SIMILARITY.
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372402AAD8B067CC CRC64;
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                        -----NYQNMIESIDENGIVTVNED
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Q52551;
Q1-NOV-1996
Q1-NOV-1996
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00034; cytochrome_c; 1.
Pfam; PF01011; Bacterial_PQ0; 6.
PROSITE; PS00190; CYTOCHROME_C;
SEQUENCE 644 AA; 69324 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular Cloning and Nucleotide sequence a Gene that Encoding Poly(vinyl alcohol) Dehydrogease from Pseudomonas sp. 113P3."; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                           222
                                                                                290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsumiya A., Hatamaka T., Tsuji M., Takakura K., Takizawa
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GEEGDETWGNDYEARWMTGAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNT: | : | : ::
                                                                                                                                                                                                                                                                                            KLKLKWA-FQYPGSKNGQATVIGDRLFTTSTSGAVYALNAKTGCVYWRHRRSEARTSPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWASAGALALLAAPAFAQV-TPVTDELLANPPAGEWISYGQNQENYRHSPLTQITTENVG 65
                                                                           DGKIYVPISSG-TEAFAQIPTWECCKFR--GALVA-LDAATGKILWKRYTTEQEPRPFKL 345
                                                                                                                             QGEDMVSNSSGPIVANGVIVAGSTCQYSPFGCFVSGHDSATGEELWRNYFI---PR---A
                                                                                                                                                                                  AALPE-----ARHKTALFFSDFTKAAVALDAETGKQLWKTVVDDQPALQMTGSITYW
                                                                                                                                                                                                                                    ATLNSFGEPTRGMALYGTNVYFVSWDNHLVALDTATG-------
                                                                                                                                                                                                                                                                                                                                                 QLQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQ----LPNI 121
                                                                                                                                                                                                                                                                                                                                                                                                   IWGNSVEGTPLDAPQCSSAPTPV--DLGA---ANQWNGWSTEKDNGRFQRKPALDVADIP 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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 Query Match
Best Local Similarity
                                                                                                                                                                                                                     MEDLINE=20208557; pubMed=10746768;
Shimao M., Tamogami T., Kishida S., Harayama S.,
"The gene pvaB encodes oxidized polyvinyl alcoho
Pseudomonas sp. strain VM15C and forms an operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
PQQ-DEPENDENT POLYVINYL
                                                                  Signal; Oxidoreductase; PQQ. SIGNAL 1 33
                                                                                                                                                                              alcohol dehydrogenase gene pvaA.";
Microbiology 146:649-657(2000).
EMBL; D50670; BAA09321.1;
                                                                                                                                                                                                                                                                                                                             quinone-dependent poly(vinyl alcohol) dehydrogenase
strain VM15C.";
                                                                                                                                                                                                                                                                                                                                  STRAIN=VM15C
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                                                                                                                                                                      EMBL; AB008494; BAA94193.1; -.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96376165; PubMed=8782398;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria
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                                                                                          PROSITE;
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                                                                                                                                            InterPro; IPR002372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTDRYFRALSQETGETLWQ----TRLATVASGQAISYEVDGMQYVAIAGGGVSYGSGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQEFTSMDVYNTSN 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYLQEDGGRKGVSPCR----AEIGHDLRARFRPTRARRFWE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVL----TGV-PCKTGTMWQFDAETGEFLWA--RDTNYQNMIESIDENGIVTVNEDAI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VMAIDADTGAVRWTVQLLADDNYIDGCW------QKGKEHANCPNPLGPDFSIGRA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -RQLSL-----GSALGGMEFGTAA---DDGKVYAGVSDIA--SQAKDRG------
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                                                                                      PF00034; cytochrome_c; 1.
PF01011; Bacterial_PQQ; 5.
TE; PS00190; CYTOCHROME_C; 1.
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                                                    68049 MW;
9.0%;
22.4%;
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02, Last sequence update)
15, Last annotation update)
ALCOHOL DEHYDROGENASE PRECURSOR
 Score Pred.
                                                               POTENTIAL
                                                 406E9EF873963B8A CRC64;
 276.5; DB 2; No. 2.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639
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             Length 639;
                                                                                                                                                                                                                      polyvinyl
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030326;
01-JAN-1998
01-JAN-1998
01-JUN-2000
                                   dehydrogenase complex from Acetobacter europaeus.";
Arch. Microbiol. 168:81-91(1997).
-!- CATALYTIC ACTIVITY: D-GLUCOSE + ACCEPTOR = D-GLUCONO-1.5-I
                                                                                                                                                                                                  Bacteria; Proteobacteria; Gluconacetobacter.
                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
GLUCOSE DEHYDROGENASE-A [PYRROLOQUINOLINE-QUINONE]
               <del>-</del>
                                                                                         Thurner C.A., Vela C., Thoeny-Meyer L., Meile L., "Biochemical and genetic characterization of the a
                                                                                                                                                                                                                                Acetobacter europaeus
                                                                                                                                                                                                                                                 GDHA.
                                                                                                                       MEDLINE=97385083; PubMed=9238099;
                                                                                                                                        STRAIN-DSM 6160;
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                   NCBI_TaxID=33995;
                                                                                                                                                                                                                                                              (QUINOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    604
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   SUBUNIT:
               COFACTOR:
                              + REDUCED ACCEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                    GMVYVHSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGVSYGSGLNSALAGERVDSTA----IGNAVYVFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAMPGVVFAGSMDGHFRAFSTSDGKVLWEFNTAAAPYKTVAGKQADGGVMDGAG-PTIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGGGVLFNGGTDRYFRALSQETGETLWQTRLA----TVASGQAISYEVDGMQYVAIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMDVY-NTSNVTKLPPGKDMIGRIDAIDISTGRTLWS--VERAAANY-----SPVL 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNAATGERRVL - - - - - - TGVPCKTGTMWQFDAET - GEFLWARDTNYQNMIESIDENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQLPAGAPAQYA--IFFSDWTKAAVALDAQTGKQLWKTTIDDQPGVQMTGSPTYHEGKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGEPTRGMALYGTNVYFVSWDNHLVALDTATG----QVTFDVDRG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LWASAGALALLAAPAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQITTENVGQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --NVYVGISDVITRKGGKP---GVYALRIRDGADVWAFPAPRTPCRWNNIFCHPAVSQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPDSGIYFIPLNNVCYDMMAVDQEFT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDFALGNSPILHTLQDGRQYIVVGQKSGAVYAMDPDNDGELIWMR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IWGPPSASMPLDGPKCKGKIPPID--LSTP--DQWNGWGAGITNARFQPNPGLTAADVPR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143;
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(BY SIMILARITY).
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Search completed: August 8, 2001, 19:43:52 Job time: 194 sec
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-!- SIMILARITY: STRONG TO OTHER PQQ GLUCOSE DEHYDROGENASE, LOT
METHANOL DEHYDROGENASE SUBUNITS 1, AND TO A.ACETI ETHANOL
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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FILLING DATE: 20-MAR 1990 ATTORNEY AGENT INFORMATION: NAME: GOODMAN, HERDERT REGISTRATION NUMBER: 17081 REFERENCE/DOCKET NUMBER: 910134/HG REFERENCE/DOCKET	10016-20 READABLI TYPE: ER: IBM ING SYSTI ARE: ASC APPLICATION PLICATION PLI	985-458-1 pence 1 Application int No. 5344777 int No. 5344777 pelicant: Tamaki, T peplicant: Takemura, peplicant: Takemura, peplicant: Kawamura, peplicant: Kawamura, peplicant: Kawamura, pelicant: Kawamura, peplicant: Kawamura, peplicant: Newention: TITLE OF INVENTION: TITLE OF INVENTI
	-9801 ES)	US/07985458 Oshimi; Hiroshi; enji; enji; enji; enji; enji; enji; enjine and Yoshiya Structural Gene of Membrane-Bound Structural Gene of Membrane-Bound Alcohol Dehydrogenase Complex, Plasmid Containing The Same And Transformed Acetic Containing The Same And Transformed Acetic Alcohol Lehydrogenase And Transformed Acetic Containing The Same And Transformed Acetic High Holtz, Goodman & Woodward, P.C. Avenue

Acid

ORIGINAL

ORGANISM:

Acetobacter altoacetigenes

MOLECULE TYPE

-+FE: genomic DNA SOURCE:

TOPOLOGY: unknown

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GENERAL INFORMATION:
APPLICANT: Choi, Eui-Sung
APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase,
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
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AUTHORS: Fukaya, Masahiro;
AUTHORS: Fukaya, Masahiro;
AUTHORS: Tayama, Kenji;
AUTHORS: Tayama, Kenji;
AUTHORS: Kokumura, Hajime;
AUTHORS: Kokumura, Hajime;
AUTHORS: Nishiyama, Makoto;
AUTHORS: Nishiyama, Makoto;
AUTHORS: Horinouchi, Sucharu and
AUTHORS: Beppu, Teruhiko
TITLE: Cloning and Sequencing of the Gene Cluster
TITLE: Cloning Two Subunits of Membrane-Bound
TITLE: Alcohol Dehydrogenase from Acetobacter
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PAGES: 1991
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Pred. No. 1.2e-13;
0; Mismatches 178; Indels 6
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; ORGANISM: Gluconobacter suboxydans
US-09-296-284-1
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; TYPE: DNA
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-22
                                                                                                                                                               Query Match
Best Local Similarity
Matches 212; Conserv
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Choi, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09296284A Patent No. 6204040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Choi, Bui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of Use Thereof
FILE DEFENDENCE: 1523 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.4%; Score 76.2; DB 4; Best Local Similarity 52.9%; Pred. No. 9.5e-10; Matches 212; Conservative 0; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/296,284A CURRENT FILING DATE: 1999-04-22 NUMBER OF SEQ ID NOS: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
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                                                                                          100 GCGAACCCCGCCCGCTGGTGAATGGATCAGCTACGGTCAGAAACCAAGAAAACTACCGTCAC 159
160 TCGCCCCTGACGCAGATCACGACTGAGAACGTCGGCCGACTGCAACTGGTCTGGGCGCGC
                                                                130 gccgaccagcatccgggtgactggatgagctatggccggacctattccgagcagcgctac 189
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52.98;
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                                                                                                                                                                                  Score 76.2; DB 4;
Pred. No. 9.6e-10;
                                                                                                                                                               Mismatches 183;
                                                                                                                                                                                                    Length 2265;
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1154 gccctggatgccaagaccggcaagctggtctggagcgtcta 1194

454 GCCCTCGACACCGCAACTGGCCAAGTGACGTTCGACGTCGA 494

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CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
FENTS: 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 212; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Gluconobacter suboxydans
1094 cgtggtgcagcctactggaacggcaaagtctatttcggcaccttcgacggtcgcctgatt 1153
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                       394 CGCGGCATGGCGCTGTACGGCACCAACGTTTACTTTGTTTCGTGGGACAACCACCTGGTC 453
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                                                                                                                                                                                                                                                                                                 220 GGCATGCAGCCGGGCAAAGTCC---AAGTCACGCCCCTGATCCATGACGGCGTCATGTAT 276
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                                                                                                                                                                                                          CTGGCAAACCCGGGCGACGTGATCCAGGCCATCGACGCCAAAACTGGGCGATCTGATCTGG
                                                                                         tcttacgatccaaaggttccaggcaacatcgccgaccgcggctgctgcgatacggtcaac
                                                                                                                                                                                gccaccacaaactggagcaagatgaaggctctggatgcagctacgggcaagctgctgtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                      gccgaccagcatccgggtgactggatgagctatggccggacctattccgagcagcgctac 853
                                                                                                                                      GAACACCGCCGAACTGCC---GAACATCGCCACGCTGAACAGCTTTGGCGAGCCGACC
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52.9%;
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                                                                                                                                                                                                                                                                                        Matches 152;
                                                                                                                                                                                                                                                                                                          Query Match 2.4%;
Best Local Similarity 45.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2745 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
1165 GATGCGATCCTGAAGGAACTGGATGTTGAATATGACGTCTGCCCGACCTTCTTGGGCGGC
                                                           1126 ACCAAGCCACGGGCGCCCAAGGATGCCCCAGCACGAAGCCGCAACGGATCCCGAGGACGCC 1185
                                                                                               1105 ACCAACTACCAGAACATGATCGAATCCATCGACGAAAACGGCATCGTGACCGTGAACGAA 1164
                                                                                                                                     1066 AAGACCCGCCGCCGCCAAATCCGCCGCCGCGAAGGCACCGTCGGCCCGCGGCCACGCG 1125
                                                                                                                                                                         1045 AAAACCGGCACCATGTGGCAGTTCGACGCCGAAACCGGCGAATTCCTGTGGGCCCGTGAT 1104
                                                                                                                                                                                                            1006 CGGTCCGTCAAGCCCGCCTCGGCACCCCAGGACACTACGACCAGCACCATCCCGAAAAAGG 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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CLASSIFICATION: 435 -
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de LISLE, GEOFFREY W.
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BLOOM, BARRY R.
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Pred. No. 0.18;
0; Mismatches 183;
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US-08-363-255-13
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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TELECOMMUNICATION INFORMATION:
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APPLICANT: BLOOM, BARRY R.
APPLICANT: COLLINS, DESMOND M.
APPLICANT: GELISLE, GEOFFREY W.
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                                                                              FEATURE:
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ATTORNEY/AGENT INFORMATION:
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LOCATION: replace(937, "")
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VENTION: MYCOBACTERIA VIRULENCE FACTORS AND A
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STREET: New Jersey
STATE: New Jersey
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APPLICANT:
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                   MOLECULE TYPE:
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HYPOTHETICAL:
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                                                       STRANDEDNESS:
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; STRAIN: ATCC
US-08-471-119A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                              TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-D
SOFTWARE: ASCI(DOS) TE
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROSteck, Paul K., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-1
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                                                                                                                                                      TELECOMMUNICATION INFORMATION:
FEATURE:
                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
CITY: I
                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                  TOPOLOGY:
                                                  STRANDEDNESS:
                                                                                  LENGTH:
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                                                                nucleic acid
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                                                                                                                                                                                                                                                                                                            ASCI(DOS) Text only
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TCC 34921
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47.8%;
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Pred. No. 0.2;
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US-08-804-198-1

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Sequence 1, Application US/08804198 Patent No. 5945320

GENERAL INFORMATION:

Burgett, Stanley Burgett, Stanley G. Kuhstoss, Stuart A. Rao. Nagarata Rao, Nagaraja R. Richardson, Mark A.

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

APPLICANT:

CANT: Rosteck, OF INVENTION:

Paul R., Jr PLATENOLIDE

SYNTHASE GENE

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Best Local Similarity 41.8%;
Matches 246; Conservative
1177 GGAGGCGGTGCTCCGGGCCGGCCTGCGCCCAGGCCCGGGTCGACCCCGCC 1225
                                      1674 GGCTGGCGAGCGAGTCGACTCGACCGCCATCGGTAACGCCGTCTACGTC 1722
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                                                                                                                           GCAATATGTCGCCATCGCAGGTGGTGGTGTCAGCTATGGCTCGGGCCTGAACTCGGCACT 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGGATATGATCGGTCGTATTGACGCGATCGACATCAGCACGGGTCGTACGCTGTGGTC 1433
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                                                                                   CGTCGCCGTCGGCAACGACGGCGGCGGCCCCGGGCTGACCGCTCCCGACCGCGAGGGACA
                                                                                                                                                                      CCTGAAGCCCCTCGCCGACGCCCTGGCCGACGGGGACCCCGTGTACTGCGTGGTGCGTGG
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                                                                                                                                                                                                                                                                                                                                          CGCCGACGAGGGAACGCCCATGGAACGCCTCGGCGCGCTGTCACCCGACGGCCGCTG
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31329..36071
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350..14002
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20110..31284
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Pred. No. 1.2;
0; Mismatches 343;
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US-08-804-198-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    1134 CGACGAAAACGGCATCGTGACCGTGAACGAAGATGCGATCCTGAAGGAACTGGATGTTGA 1193
                                                                                                                                                                                                                     1254 CGACAGCGGCATCTACTTCATCCCGCTGAACAACGTCTGCTATGACATGATGGCCGTCGA 1313
                                                                                                                                                                                                                                                                                 1434 GGTCGAACGTGCTGCGGCGAACTATTCGCCCGTCTTGTCGACCGGCGGCGGCGTTCTGTT 1493
                                                                   1374 CAAGGATATGATCGGTCGTATTGACGCGATCGACATCAGCACGGGTCGTACGCTGTGGTC 1433
                                                                                                                                              1314 TCAGGAATTCACCTCGATGGACGTCTATAACACCAGCAACGTGACCAAGCTGCCGCCCGG 1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                    757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
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                                  CGAGAGCCTGCGGCCACCTCCCGCGTCGCCGTCGCCGGGGGCGTCAACCTGGTCCT 936
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                                                                                                           CCCCAGCCTCGCGGTCGACACCGCCCAGTCGTCCTCCCTGGTCGCCGTTGGCCCTCGCCGT 876
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LILLY CORPORATE CENTER
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Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: QUAX, WILHELMUS
APPLICANT: LUITEN, RUDOLF G.M.
APPLICANT: SCHUURHUIZEN, PAUL W.
APPLICANT: MRABET, NADIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19910110
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                                                                                                                            FEATURE:
                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Str
                                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1177 GGAGGCGGTGCTCCGGGCCGGCCTGCGCCCAGGCCCGGGTCGACCCCGCC 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1674 GGCTGGCGAGCGAGTCGACTCGACCGCCATCGGTAACGCCGTCTACGTC 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1614 GCAATATGTCGCCATCGCAGGTGGTGGTGTCAGCTATGGCTCGGGCCTGAACTCGGCACT 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1117 CGTCGCCGTCGGCAACGACGGCGGCCGGCCCGGGCTGACCGCTCCCGAACCGCGAGGGACA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1494 CAACGGTGGTACGGATCGTTACTTCCGCGCCCTCAGCCAAGAAACCGGCGAGACCCTGTG 1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           997 CCACACCTTCGACGCCCGTGCCAACGGCTATGTCCGCGGTGAGGGCGGCGCCGCCGTCGT 1056
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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LOCATION: 1..1164
IDENTIFICATION METHOD:
                                                                                   NAME/KEY:
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Menlo Park
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; OTHER INFORMATION:
US-07-640-476-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                    ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,
                                                                                                                                                                SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Horowitz, Jeannine
APPLICANT: Rosichan, Jeffrey L.
TITLE OF INVENTION: AN EXPRESSION CONTROL SEQUENCE FOR
TITLE OF INVENTION: GENERAL AND EFFECTIVE EXPRESSION OF GENES IN PLANTS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 CCGCGGCGACATCCTGCTGCCCACCGTCGGCCACGCCCTGGCCTTCATCGAGCGCCTGGA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 CCCGGGCGACGTGATCCAGGCCATCGACGCCAAAACTGGCGATCTGATCTGGGAACACCG 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             861 CTTCAAGCCGCCGCGGACCGAGGACTTCGACGGCGTGTGGGCCTCGGCCGCGGGCTGCAT 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    519 TTCGAACTCGTCGGCCCGATCGTGGCAAACGGCGTGATCGTTGCCGGTTCGACCTGCCA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                681 CTTCCCGCACGGCATCGCGCAGGCCCTGTGGGCGGGCAAGCTCTTCCACATCGACCTCAA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   FILING DATE: 26 CLASSIFICATION:
                                                                                                                    APPLICATION NUMBER: US/08/686,417 FILING DATE: 26-JUL-1996
                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGTTCTGGCTGGTCGACCTCCTGGAGACCGCCGGTTACGAGGGCCCCGCGGCACTTCGA
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                                                                                                                                                                                                                                                                                                                                                      Washington
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                                                                                                                                                                                                                                                                                                                                                                         2000 Pennsylvania Avenue, NW
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                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbour, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baszczynski, Chris
                                                                                                                                                                                     PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                               MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.3%;
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/product= "xylose isomerase (glucose isomerase)"
/evidence= EXPERIMENTAL
/standard_name= "D-xylose ketol isomerase"
                                      29,959
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                       27112-20038.00
                                                                                                                                                                                          Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1164;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                     APPLICANT: Wilson, James M. APPLICANT: Farina, Steven F. APPLICANT: Fisher, Krishna J.
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/923,137
                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     671 AGGGTGATGAGACTTGGGGCCAACGATTACGAAGCCCGTTGGATGACCGGTGCCTGGGGCC 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580 ACGCGTCCGCTGCAGCGTTGGCGTACAGGCCGGACTACATTAGCCAACGCGTATCGGCAG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           700 CCCTCCGCTACTCCTCCTCCCCACCCCACTCCCCGCAGGAGCGGCGGCGGCGGCGGCGA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 731 AGATCACCTATGACCCCGTCACCAACCTTGTCCACTACGGCTCGACCGCTGTGGGTCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              911 GGGACCAGGAATGCACGTTCGAGATGATGGTCACCAATGTGGATGTCCAACCCTCGACCG 970
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940 ACAAGGGCGTGACCCCGAGAAGGTCCGGACCACCCCCTCT 980
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                                                                                                                                                              CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                      OPERATING SYSTEM:
                                                                       COMPUTER:
                                                                                        MEDIUM TYPE:
                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                             United States of America
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2970..3167, 3250..3573)
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                                                  E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.
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FILING DATE: CLASSIFICATION:

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; LOCATION: (539)..(4600)
US-09-398-193-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 98
LENGTH: 5515
THE TENT OF THE TENT
                                                                                                                                                                                                            Query Match 2.2%;
Best Local Similarity 44.0%;
                                                                                                                                                                               Matches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 98, Application US/09398193 Patent No. 6197581
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TITLE OF INVENTION: Adenylate cyclase and uses therefor
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20465 GCTCCTGACGCCCAACGAGTTCGAAATCA 20493
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3632 ctgaggaacatcatcccctaccacgtggctgagcagctgaaggtgtcccagacctactcc 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1383 GATCGGTCGTATTGACGCGATCGACATCA 1411
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                                                                             982 CTGCAGTCGATCAACCCGAACGCCGCAACTGGCGAGCGTCGCGTGCTGACCGGCGTTCCG 1041
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
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PRIOR APPLICATION UNBER: US 60/024,700
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bak, Mary E.
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                                                                                                                                                                                                        Score 39; DB
Pred. No. 1.3;
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Pred. No. 1.7;
0; Mismatches 106; Indels
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                                                                                                                                                                   Mismatches 210;
                                                                                                                                                                                                                                            DB 4; Length 5515;
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US-07-642-734C-3
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Patent No. 582451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                         TELEFAX: 708-938-2623 INFORMATION FOR SEQ ID NO:
                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pai
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                  TELEPHONE: 708-937-9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Recombinant DNA Metho
                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Donadio, S
APPLICANT: Mcalpine,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1162 GAAGATGCGATCCTGAAGGAACTGGATGTTGAATATGACGTCTGCCCGACCTTCTTGGGC 1221
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
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STRAIN:
                      ORGANISM:
                                                                                                                               TOPOLOGY:
                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                         nucleic acid
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NRRL 238
                                                                                                                                                                                      20235 base pairs
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Abbott Laboratories D377/AP6D-2 One Abbott
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                  Saccharopolyspora erythraea
                                                                                      NO
                                                                                                      DNA (genomic)
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OTHER INFORMATION: /codon_start= 19
OTHER INFORMATION: /function= "gene eryA"
OTHER INFORMATION: /product= "eryA ORF2 encoding modules
OTHER INFORMATION: 6-deoxyerythronolide B"
FEATURE:
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OTHER INFORMATION: /function= "approximate span c
OTHER INFORMATION: acyltransferase domain module
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LOCATION:
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LOCATION: 4471.5847
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoacylaCPsynhase domain of module"
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OTHER INFORMATION: /functi
OTHER INFORMATION: module
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OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: beta-ketoreductase domain of
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OTHER INFORMATION:
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                                                                                                    OTHER INFORMATION: /codon_start= 10723
OTHER INFORMATION: /function= "gene = eryA"
OTHER INFORMATION: /product= "orf3 encoding modules 5 &
OTHER INFORMATION: 6-deoxyerythronolide B formatio"
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /function= "approxi OTHER INFORMATION: beta-ketoreductase
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LOCATION:
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LOCATION:
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OTHER INFORMATION:
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                       OTHER
YKEY: misc_feature
TION: 10723..15165
R INFORMATION: /func
R INFORMATION: modul
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19..10722
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10723..20235
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9433..9984
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6054..7026
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beta-ketoacyl ACP synthase of module 3"
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module 3"
  /function=
module 5"
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module 4"
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beta-ketoreductase of module
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                     "approximate span of
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module 3"
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OTHER INFORMATION: /funct
OTHER INFORMATION: beta-k
FEATURE:
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Best Local
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OTHER INFORMATION: /func OTHER INFORMATION: acyl FEATURE:
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                                                                                                                                                                                                                              6304 GTGACCCCGGCCGCCGTCGTCGCCACTCGCAGGGCGAGATCGCCGCGGCGCACGTGGCG 6363
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                                                                                                                                                                                                                                                                335 GGGAACACCGCCGCCAACTGCCGAACATCGCCACGCTGAACAGCTTTGGCG-AGCCGACC 393
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LOCATION: 10831..12174
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
                                    514 ATGGTTTCGAACTCGTCGGGCCCGATCGTGGCAAACGGCGTGATCGTTGCCGGTTCGACC 573
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LOCATION:
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LOCATION: 18379..18921
OTHER INFORMATION: /fun
OTHER INFORMATION: beta
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LOCATION: 15166..20235
OTHER INFORMATION: /function-
OTHER INFORMATION: module 6"
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Local Similarity 45.9%;
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LOCATION: 19492..20235
OTHER INFORMATION: /function= "approximate span c
OTHER INFORMATION: thioesterase domain of module
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                                                                                              GCCCTCGACACCGCAACTGGCCAAGGTGACGTTCGACCGCGGCCCAAGGCGGAAGAC 513
GTGCTCGCGCGCTGGGACGGCCGTGTCGCCGGTGGCCGCCGTGAACGGGCCTGGCACCAGC 6543
                                                                        GAGCTCGACGACCAGGGCGGCATGGTCGGTCGGCGCGTCCCGCGACGAGGTGGAGACC 6483
                                                                                                                                                                                        CGCGGCATGGCGCTGTACGGCACCAACGTTTACTTTGTTTCGTGGGACAACCACCTGGTC 453
                                                                                                                                                                                                                                                                                                          168;
                                                                                                                                                                                                                                                                                                        Conservative
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12379..13350
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19149..19398
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beta-ketoacylACPsynthase domain of modul"
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beta-ketoreductase of module
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acyl carrier domain of module 6
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beta-ketoreductase domain of module
                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                          Score 38.8;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 847-938-3137 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Method of Directing Biosynthesis TITLE OF INVENTION: Specific Polyketides NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Katz, L
APPLICANT: Mcalpine, J B
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                                                   NAME/KEY: misc_feature LOCATION: 19..4470 OTHER INFORMATION: /fur
                                                                                                                                                           LOCATION: 19..10722
OTHER INFORMATION: ,
OTHER INFORMATION: ,
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                                                                                                                                                                                                                                                 UKGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 11-MAY-1995 CLASSIFICATION: 435
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                                  OTHER INFORMATION:
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                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 19.
NAME/KEY:
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for 6-deoxyerythronolide B"
                                    module
                                  /function=
module 3"
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LOCATION: 10723..20
OTHER INFORMATION:
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LOCATION: 10723..1:
OTHER INFORMATION:
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                                                          OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 10225..1
OTHER INFORMATION:
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OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoacylACPsynhase domain of module"
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LOCATION:
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    LOCATION:
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misc_feature
14062..14610
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10723..15165
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10723..20235
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4471..5847
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acyltransferase domain of module
                                                          /function= "approximatr span of
acyltransferase domain of modul
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/product= "orf3 encoding modules 5 & 6
6-deoxyerythronolide B formatio"
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module 4"
                                                                                                                                                                                                                                                              module
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dehydratase and enoylreductase domains m"
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beta-ketoacylACPsynthase domain of modul"
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module 5"
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beta-ketoacyl ACP synthase of module
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; NAME/KEY: misc_feature; COATION: 19492..20235; OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: thioesterase domain of module 6" US-08-439-009a-3
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Best Local Similarity
Matches 168; Conserv
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NAME/KEY: misc_feature
LOCATION: 18379..18921
OTHER INFORMATION: /func
OTHER INFORMATION: beta-
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6664 GAGGAC 6669
                                                                                                   6604 ATGAAGCCGCGCGGATCGCCGTGCGCTACGCCTCCCACTCCCCGGAGGTGGCGCGCATC 6663
                                                                                                                                                                                                       6544 GTCGTTGCCGGGCCGACCGCGGAGCTGGACGAGTTCTTCGCCGAGGCCGAGGCGCGGGAG
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                                                                                                                                                                                                                                        574 TGCCAATACTCGCCGTTCGGCTGCTTTGTCTCGGGCCACGACTCGGCCACCGGTGAAGAG 633
                                                                                                                                                                                                                                                                                                                                            514 ATGGTTTCGAACTCGTCGGGCCCGATCGTGGCAAACGGCGTGATCGTTGCCGGTTCGACC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 CGCGGCATGGCGCTGTACGCCAACGTTTACTTTGTTTCGTGGGACAACCACCTGGTC 453
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                                               694 GATTAC 699
                                                                                                                                                     634 CTGTGGCGCAACTACTTCATCCCGCGCGCTGGCGAAGAGGGTGATGAGACTTGGGGCCAAC 693
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LOCATION: 19149..1938
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
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LOCATION:
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LOCATION: 16768..17721
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
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LOCATION: 15172..16569
OTHER INFORMATION: beta-ketoacylACPsynthase domain
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LOCATION: 15166..20235
OTHER INFORMATION: /fur
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14857..15114
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module 6"
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beta-ketoreductase domain of module 6"
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beta-ketoreductase of module 5"
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Pred. No. 2.1;
0; Mismatches 197; Indels 1;
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Search completed: August 9, 2001, 22:38:11 Job time: 44890 sec

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Post-processing: Minimum Match 0%
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Maximum DB seq length: 2000000000
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Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X. Genetic snapshots of the Rhizobium species NGR234 genome GenomeBiology.com 1 (6), 0014.1-0014.7 (2000)
Contact: Virginie Viprey
                                     Rhizobium sp. NGR234
Rhizobium sp. NGR234
Bacteria; Proteobacteria;
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                                                                       sp. NGR234 genomic clone 04g03,
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fruit fly.
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS0091P 925 bp DNA GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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University of Geneva
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ANU265"
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                Cypriniformes; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 643)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter, E., Swaller, T., Gibbons, M., Pape, D., Harvey, M., McCann, R., Warberston, R.
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Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
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/note="end : TET3"
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Library constructed by: Susan E. Brockerhoff DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
Contact: Stephen L. Johnson
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                    BG307693 667 bp mRNA EST 22-FBB-2001 fm519(3).yl Zebrafish adult retina cDNA Danio rerio cDNA clone 4199212 5' similar to SW:GBB1_HUMAN P04901 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1 ;, mRNA
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/note="Vector: Lambda AAP II (pBluescript SK-); Site_1:
ECORI; Site_2: SalI; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
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/db_xref="taxon:7955"
/clone="4200605"
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                                                                    CNS0091P 925 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/lab_host="E.Coli XLI-Blue MRF')"
/lab_host="E.Coli XLI-Blue MRF'); Site_1:
/note="Vector: Lambda ZAP II (pBluescript SK'); Site_1:
EcoRI; Site_2: SalI; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
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/clone="4199212"
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                                                                                                                                                                                                                                                                                                                                                                                                      Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fi
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1 (bases 1 to 925)
                        AW827060 616 bp mRNA EST fk57h09.y1 Zebrafish adult retina cDNA Danio to gb:X04526_cds2 GJANIE NUCLECTIDE-BINDING
BETA SUBUNIT (HUMAN);, mRNA sequence.
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/note="Vector: Lambda 2AP II (pBluescript SK-); Site_1:
BCORI; Site_2: SalI; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
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                                              TGATAACCAGATTGTGACCAGCTCAGGCGACACCACCTGTGCTCTGTGGGACATCGAGAC
                                                                                                                                      GCGCGTCAGCCGCGAGCTAGCCGGACACACAGGTTATCTGTCCTGCTGTTCCTTGGA
                                                                                                                                                                                                                                     GTGCGGAGGTTTGGACAACATCTGCTCCATCTACAACCTGAAGACCCGCGAGGGGAACGT
                                                                                                                                                                                                                                                                              CTTTGTTTCGTGGGACAACCACCTGGTCGCCCTCGACACCGCCAACTGGCCAAGTGACGTT 485
                                                                                                                                                                                                                                                                                                                               CCCGCTGCGCTCCTCGTGGGTGATGACCTGTGCGTACGCGCCGTCCGGGAACTACGTGGC 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: zbrafish@watson.wustl.edu
Library constructed by: Susan E. Brockerhoff DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kohn,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop:
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www.rzpd.de)
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/lab_host="E.Coli XLI-Blue MRF')"
/lab_host="E.Coli XLI-Blue MRF')"
/note="Vector: Lambda ZAP II (pBluescript SK-); Site_
ECORI; Site_2: SalI; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
a 175 c 194 g 132 t
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/db_xref="taxon:7955"
/clone="4199547"
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                                                                                                                                                                                                         CTACAACCTCGTCACCGACATCTACGAGTGGGGCCTGGGGGCCAGTCCTTCCCACTTCTCGCC 237
                                                                                                                                                                                                                                         CCAGGCCATCGACGCCAAAACTGGCGATCTGATCTGGGAACACCGCCGCCAACTGCCGAA 359
CATGCGCGCCATCGCCGCCCACTACGGCGCCCACTTGGTCGGCATCACCATCAACGAGTA 417
                               GACGTTCGACGTCGACCGCGGCCAAGGCGAAGACATGGTTTCGAACTCGTCGGGCCCGAT 539
                                                                                                  CGTTTACTTTGTTTCGTGGGACAACCACCTGGTCGCCCTCGACACCGCAACTGGCCAAGT 479
                                                                                                                                       CTCCCTCCCGGCCGCTCCCACCGCGACGCCACCGCGTCCACGAGGAGCGCGTCGCCGA
                                                                 CCTGCTCGCCGACAGGCCGGGCCACCGCGTGCTCGACGTCGGATGCGGCGTCAGCGTGCC 357
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HVSMEh0100C21f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0100C21f,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Ram
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
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864 656 4293
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Hordeum vulgare 5-45 DAP spike HVcDNA0009 (5 to 45 DAP)" (tissue_type="5-45 DAP Spike" /tissue_type="5-45 DAP Spike"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare"
/cultivar="Morex"
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719 GTGCCTGGGGCCAGATCACCTATGACCCCGTCACCAACCTTGTCCACTACGGCTCGACCG 778
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CTGTGGGTCCGGCGTCGGAAACCCCAACGCGGCACCCCGGGCGCACGCTGTACGGCACGA 838
                                                   ACACCCGTTTCGCGGTGCGTCCTGACACGGGCGAGATTGTCTGGCGTCACCAGACCCTGC 898
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
132I16 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cms.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="G"
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PUC-Ori"
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/db_xref="taxon:99883"
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b; Pred. No. 1;
44; Mismatches 91;
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                                                                   397 GGCATGGCGCTGTACGGCACCAACGTTTACTTTGTTTCGTGGGACAACCACCTGGTCGCC 456
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                                                                                                                                                                                                                                                                                        277
                                                                                                                                                                                                                                                                                                                                                                               217 CGCGGCATGCAGCCGGGCAAAGTCCAAGTCACGCCCCTGATCCATGACGGCGTCATGTAT 276
                                                                                                                                                                                                                                                                                                                                         ω
                  GGCCAGAAGGTGAAGGTCGTGCTGGCTGCCGCCACCTGGCAGAACCCCCACCTGATCGTG 242
                                                                                                                                                                                                                                                                              CTGGCAAACCCGGGCGACGTGATCCAGGCCATCGACGCCAAAACTGGCGATCTGATCTGG 336
                                                                                                                                                                                                                                                                                                                                 CGCGACACCCTGGTGGAGCTGGGCTACGAGAAGCTGGTGAACGAGCTGGACATCAAGGAG 62
                                                                                                                         GAGGACCTGGGCCTGGAGTCGGAGTTCGCCCTGCACAGCCACATTCGCGGCCTGTCGGGC
                                                                                                                                                                                                                             GCCGCCGCGCTGGGCCTGTTCACCCGCCCGCCTCACCACCGCCTCGATCCAGAAGCACCTG
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894024H07.yl C. reinhardtii CC-1690,
Chlamydomonas reinhardtii cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. PBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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/db_xref="taxon:3055"
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                                             TCGAGAAGGCCGGCGTGGCGCACAAGATCGACTTCCGCGAGGGCCCCGGCGCTCCCCGTCC
                                                                                        CCGAGATGGAAGGTCTGCAGTCGATCAACCCGGAACGCCGCAACTGGCGAGCGTCGCGTGC 1027
                                                                                                                                                                                                                                                                                                                          CGGCGGACGAGGGCCAGTTCCTCAACATGCTGCTCAAGCTCATCGGCGCCCAAGAAGACCA 112
                                                                                                                                        ACGGCACCATCTTGGCCATGGACATCAACCGCGAGAACTACGAGCTGGGGGCTGCCGTGCA 232
                                                                                                                                                                                   ACTGGGACCAGGAATGCACGTTCGAGATGATGGTCACCAATGTGGATGTCCAACCCTCGA 967
                                                                                                                                                                                                                                 TGGAGATCGGCGTCTACACGGGCTACTCCCTGCTCGCCACCGCGCTCGCCATCCCCGACG 172
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Fax: 864 656 4293
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100 Jordan Hall, Clemson, SC 29634, USA
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Ram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Nov 16, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVSMEf0019H19f Hordeum vulgare seedling root EST library HVcDNA0007 (etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0019H19f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="HVSMEf0019H19f"
/clone_lib="Hordeum vulgare seedling root EST library
/clone_lib=Hordeum vulgare seedling root EST library
HVCDNA0007 (ettolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TyC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1"
282 c 184 g 133 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; I
Pred. No. 1
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Mismatches
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                                                                                                                                                                                          BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1208 CGACCTTCTTGGGCGGCCGCGACTGGCCGTCGGCCGCACTGAACCCCCGACAGCGGCATCT 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1148 TCGTGACCGTGAACGAAGATGCGATCCTGAAGGAACTGGATGTTGAATATGACGTCTGCC 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1088 TCCTGTGGGCCCCGTGATACCAACTACCAGAACATGATCGAATCCATCGACGAAAACGGCA 1147
1029 GACCGGCGTTCCGTGCAAAACCGGCACCATGTGGCAGTTCGACGCCGAAACCGGCGAATT 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 GCCTCCTCGGCTACGACAACACCCTCTGGAACGGCTCCGTCGTGCTCCCCCGCCGACGCCC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 CCGCCGACCAGCGCGTNGAGATCTGCCAGCTCCCCGTCGGCGACG 577
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                                                                     Match 2.5%;
Local Similarity 47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVSMEg0019P18f Hordeum vulgare pre-anthesis spike EST library HVcDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone HVSMEg0019P18f, mRNA sequence.

BE456143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
On Jul 26, 2000 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Ram,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. a.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rwing@clemson.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 550.
                                                 Conservative
                                                                                                                                                                                                                                                                                   /db_xref="taxon:4513"
/clone="HVSMEg0019p18f"
/clone=lib="Hordeum vulgare pre-anthesis spike EST library
/clone_lib="Hordeum vulgare pre-anthesis spike EST library
HVcDNA0008 (white to yellow anther)"
                                                                                                                                                                                            /note="Vector: lambdaZAP; Site_1: EcoR1;
296 c 233 g 150 t 25 others
                                                                                                                                                                                                                                    /tissue_type="pre-anthesis spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                            Score 42.8; DB 167; Pred. No. 1.6; 0; Mismatches 182;
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                                                                                                DB 167; Length 880;
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                                                                                                                                             BASE COUNT
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Query Match 2.4%;
Best Local Similarity 48.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1329 GATGGACGTCTATAACACCAGCAACGTGACCAAGCTGCCGCCCGGCCAAGG 1378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 CCCCGACCTGGCTCCCATCAAGAAGGGGCCCCAGCTGCCGCCCACCCCGG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 GCTCAAGTTCCTGCTCATCGGCGGCGCGCTCCCTGGTCGCCTACGTCAGCGCATTCGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 CGGCCTGCAGAGCAAGTTCTTCAACACCTTCGCCGCGCCCTTCACCAAGCGCGGCCTGCT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 CGGGGCGGCGGTGGTGGCCAAGTACGGGGAGAAGAGCGTGTACTTCGACCTGGACGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. plate: LLCM1047 row: g column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 767)
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                                                                                                                                             ø
                                                                                                                                    for average insert size 1.8kb. Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 221 c 251 g 150 t
                                                                                                                                                                                                                                                                 /lab_host="DH10B (phage-resistant);
/note="organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(6). Size-selected > Sf
for average insert size 1 Bkh (ibharu constructed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:4138410"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="rhabdomyosarcoma"
     Score 42.2;
Pred. No. 2.
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                                       DB 147;
                                    Length 767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Botany
The University of Georgia
Plant Sciences Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 553 POLYA=No.
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l (bases 1 to 553)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 542 1860
706 542 1805
                                                                     /note=Torgan: Anthracmose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracmose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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                                                                                                                                                                                                     High quality sequence start: 2 High quality sequence stop: 440 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                       Department of Botany
The University of Georgia
Plant Sciences Building, I
                                                                                                                                                                                                                                                                            Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions, below Phred quality 16. The threshold for highest quality sequences
                                                                                                                                                                                                                                                                                                                                         Tel: 706 542 1860 Fax: 706 542 1805
                                                                                                                                                                                                                                                     Seq primer: PolyTMix
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           An EST database from Sorghum: developing embryos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clade; Panicoideae; Andropogoneae;
1 (bases 1 to 469)
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Sorghum bicolor
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          /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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                                                                                                                                                                                                                                                                                                      328 CTGATCTGGGAACACCGCCGCCAACTGCCCAACATCGCCAACGCTTTGGCGAG 387
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